

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model  
Run on: December 30, 2004, 16:04:46 ; Search time 37 Seconds  
32.263 Million cell updates/sec

Title: US-10-718-321-1

Perfect score: 99  
Sequence: 1 SSDGLWNNTQOLFLEHS 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 150 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/pctodata/1/1aa/5A\_COMB.pep.\*  
2: /cn2\_6/pctodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/pctodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/pctodata/1/1aa/6B\_COMB.pep.\*  
5: /cn2\_6/pctodata/1/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/pctodata/1/1aa/backfilesl.pep.\*

**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	99	100.0	334	4	US-03-197-970B-7 Sequence 7, Appli
2	84.8	84.8	451	5	US-03-197-970B-7 Sequence 2, Appli
3	84	84.8	451	5	PCT-US95-09941-2 Sequence 2, Appli
4	52.5	52.5	570	4	US-03-248-796A-15079 Sequence 15079, A
5	48	48	981	4	US-03-099-258-13 Sequence 13, Appli
6	45	45.5	114	6	US-03-099-258-13 Sequence 13, Appli
7	45	45.5	114	6	US-03-099-258-13 Sequence 13, Appli
8	45	45.5	1464	1	US-03-026-138B-1 Sequence 1, Appli
9	44	44.4	590	4	US-03-538-092-967 Sequence 967, Appli
10	43	43.4	62	4	US-03-248-796A-22793 Sequence 22793, A
11	43	43	251	4	US-03-270-767-49147 Sequence 49147, A
12	43	43.4	265	4	US-03-270-767-47089 Sequence 47089, A
13	43	43.4	311	4	US-03-270-767-48661 Sequence 48661, A
14	42	42.4	187	4	US-03-248-796A-20325 Sequence 20325, A
15	42	42.4	358	4	US-03-540-236-3758 Sequence 3758, Appli
16	42	42.4	1190	4	US-03-248-796A-21474 Sequence 21474, A
17	41	41	120	4	US-03-252-991A-26719 Sequence 26719, A
18	41	41.4	155	4	US-03-268-796A-14464 Sequence 14464, A
19	41	41.4	166	4	US-03-134-000C-48688 Sequence 48688, Appli
20	41	41.4	326	3	US-03-089-397A-11 Sequence 11, Appli
21	41	41.4	326	6	US-03-539-559-2 Sequence 539559, A
22	41	41.4	365	4	US-03-248-796A-18622 Sequence 18622, A
23	41	41.4	817	4	US-03-248-796A-17089 Sequence 17089, A
24	41	41.4	1455	3	US-03-840-062-5 Sequence 5, Appli
25	41	41.4	1464	2	US-03-231-193A-11 Sequence 11, Appli
26	41	41.4	1464	3	US-03-486-273A-11 Sequence 11, Appli
27	41	41.4	1464	3	US-03-940-086A-11 Sequence 11, Appli

## ALIGNMENTS

RESULT 1  
S-03-197-970B-7  
Sequence 7, Application US/09197970B  
Patent No. 6694385  
GENERAL INFORMATION:  
APPLICANT: Michele Sanicola-Nadel  
Joseph V. Bonvouloir  
Catherine A. Hession  
Takabaru Ichimura  
Henry Wei  
Richard L. Cate  
TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSE: Biogen, Inc.  
STREET: 14 Cambridge Center  
CITY: Cambridge  
STATE: MA

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-287-001A-2

Query Match 84.8%; Score 84; DB 1; Length 451;  
Best Local Similarity 88.9%; Pred. No. 2e-05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;QY 1 SSDGILWNNNOTQLFLEHS 18  
Db 344 SSDGLWNNNOTQLSPEHS 361

RESULT 3

PCT-US95-09941-2

Sequence 2, Application PC/TUS9509941

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: HEPATITIS A VIRUS RECEPTOR AND METHODS

TITLE OF INVENTION: OF USE

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: NEEDLE &amp; ROSENBERG, P.C.

STREET: Suite 1200, The Candler Bldg, 127 Peachtree

STREET: Street

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30303

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patientin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09941

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/287,001

FILING DATE: 5 AUG 1994

ATTORNEY/AGENT INFORMATION:

NAME: Spratt, Gwendolyn D.

REGISTRATION NUMBER: 36,016

REFERENCE/DOCKET NUMBER: 1414.621

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404/688-0770

TELEFAX: 404/688-9880

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-09941-2

## GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 1017196.132

CURRENT APPLICATION NUMBER: US/09/248,76A

CURRENT FILING DATE: 1995-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15079

LENGTH: 570

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-15079

Query Match 52.5%; Score 52; DB 4; Length 570;  
Best Local Similarity 57.1%; Pred. No. 3.2; 2; Mismatches 4; Indels 0; Gaps 0;QY 2 SDGLMWNNOTQLF 15  
Db 2 NDGIWNNNDLFL 15

RESULT 5

US-09-991-258-13

Sequence 13, Application US/09991258

PATENT NO. 6783939

GENERAL INFORMATION:

APPLICANT: Olmsted, Robert

APPLICANT: Keith, Paula

APPLICANT: Dryga, Sergey

APPLICANT: Caley, Ian

APPLICANT: Maughan, Maureen

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

TITLE OF INVENTION: VACCINES

FILE REFERENCE: 0113.0013

CURRENT APPLICATION NUMBER: US/09/991,258

CURRENT FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 09/302,537

PRIOR FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: 60/216,995

PRIOR FILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13

LENGTH: 981

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Other Information: Description of Artificial Sequence; No. 6783939e =

OTHER INFORMATION: Synthetic construct

US-09-991-258-13

Query Match 48.5%; Score 48; DB 4; Length 981;

Best Local Similarity 50.0%; Pred. No. 26; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSDGLWNNNOTQLFLEHS 18  
Db 344 SSDGLWNNNOTQLSPEHS 361

RESULT 6

5514582-13

PATENT NO. 5514582

APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.

RESULT 4

US-09-248-796A-15079

SEQUENCE 15079, Application US/09248796A

PATENT NO. 6747137

TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID  
; IMMUNOGLOBULINS  
; CURRENT NUMBER OF SEQUENCES: 43  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/185, 670  
; FILING DATE: 21-JAN-1994  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 986, 931  
; FILING DATE: 08-DEC-1992  
; APPLICATION NUMBER: 808, 122  
; FILING DATE: 16-DEC-1991  
; APPLICATION NUMBER: 440, 625  
; FILING DATE: 22-NOV-1989  
; APPLICATION NUMBER: 315, 015  
; FILING DATE: 23-FEB-1989  
; SEQ ID NO:13;  
; LENGTH: 114  
; 5514582-13

Query Match 45.5%; Score 45; DB 6; Length 114;  
; Best Local Similarity 45.5%; Pred. No. 6.9; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
; Qy 2 SDGLWNNNQTCQ 12  
; Db 97 SDGLWNNDNFCCQ 107

RESULT 7

5514582-14

; Patent No. 5514582  
; APPLICANT: CARON, DANIEL J.; LASKY, LAURENCE A.  
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID  
; IMMUNOGLOBULINS  
; CURRENT NUMBER OF SEQUENCES: 43  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/185, 670  
; FILING DATE: 21-JAN-1994  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 986, 931  
; FILING DATE: 08-DEC-1992  
; APPLICATION NUMBER: 808, 122  
; FILING DATE: 16-DEC-1991  
; APPLICATION NUMBER: 440, 625  
; FILING DATE: 22-NOV-1989  
; APPLICATION NUMBER: 315, 015  
; FILING DATE: 23-FEB-1989  
; SEQ ID NO:14;  
; LENGTH: 114  
; 5514582-14

Query Match 45.5%; Score 45; DB 6; Length 114;  
; Best Local Similarity 45.5%; Pred. No. 6.9; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
; Qy 2 SDGLWNNNQTCQ 12  
; Db 97 SDGLWNNDNFCCQ 107

Query Match 45.5%; Score 45; DB 6; Length 114;  
; Best Local Similarity 45.5%; Pred. No. 6.9; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
; Qy 2 SDGLWNNNQTCQ 12  
; Db 97 SDGLWNNDNFCCQ 107

US-08-026-138B-1

Query Match 45.5%; Score 45; DB 6; Length 114;  
; Best Local Similarity 45.5%; Pred. No. 6.9; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
; Qy 2 SDGLWNNNQTCQ 12  
; Db 97 SDGLWNNDNFCCQ 107

COUNTRY: JAPAN  
; ZIP: 951  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS v.5  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/026, 138B  
; FILING DATE: 26-FEB-1993  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JP 39563/1992  
; FILING DATE: 26-FEB-1992  
; APPLICATION NUMBER: JP 173155/1992  
; FILING DATE: 30-JUN-1992  
; APPLICATION NUMBER: JP 215017/1992  
; FILING DATE: 12-AUG-1992  
; APPLICATION NUMBER: JP 303878/1992  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hamburg, C.Bruce  
; REGISTRATION NUMBER: 22-389  
; REFERENCE/DOCKET NUMBER: P-4551  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 986-2340  
; TELEFAX: (212) 953-7733  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1464 amino acids  
; TYPE: amino acid  
; STRANDBNESS: single strand  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: mouse  
; TISSUE TYPE: cerebellum  
; PUBLICATION INFORMATION:  
; AUTHORS: Masayoshi MISHINA  
; TITLE: NOVEL PROTEINS AND GENES CODING THE SAME  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 to 1464  
; US-08-026-138B-1

Query Match 45.5%; Score 45; DB 1; Length 1464;  
; Best Local Similarity 45.5%; Pred. No. 1.2e+02; Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
; Qy 1 SSDGLWNNNQTCQLEH 17  
; Db 1174 NEDGLPNNDQYKLYAH 1190

RESULT 8

RESULT 9

US-09-538-092-967

Sequence 967, Application US/9538092

Patent No. 675314

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538, 992

PRIOR APPLICATION NUMBER: 60/127, 352

PRIOR FILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/178, 965

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CurapatSeqFormatter Version 0.9

SEQ ID NO: 967

LENGTH: 590

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nishiohata Residence 1-107

STREET: 5214, Nishiohata-machi

CITY: Niigata-shi

STATE: Niigata-ken.

```

; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P20309
US-09-538-092-967

Query Match 44.4%; Score 44; DB 4; Length 590;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SDSGLWNNTQQLFLEHS 18
Db 332 SSSSWNNNDAASLENS 349

RESULT 10
US-09-248-796A-22793
; Sequence 22793, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196-132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIORITY FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO: 22793
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22793

Query Match 43.4%; Score 43; DB 4; Length 62;
Best Local Similarity 47.1%; Pred. No. 7.3;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SDGILWNNNQTQQLFLEHS 18
Db 25 SDSLQDPTVWYLPFOHS 41

RESULT 11
US-09-270-767-49147
; Sequence 49147, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 48661
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49147

Query Match 43.4%; Score 43; DB 4; Length 311;
Best Local Similarity 56.2%; Pred. No. 44;
Matches 9; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Qy 5 LWNNN--QTLFLEHS 18
Db 141 LWNNNYQKTRLFRKNS 156

RESULT 12
US-09-270-767-49147
; Sequence 49147, Application US/09270767
; Patent No. 6703491
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-49147

Query Match 43.4%; Score 43; DB 4; Length 251;
Best Local Similarity 56.2%; Pred. No. 35;
Matches 9; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Qy 5 LWNNN--QTLFLEHS 18
Db 52 LWNNNYQKTRLFRKNS 67

RESULT 12

```



NUMBER OF SEQ ID NOS: 6812  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 4868  
 LENGTH: 166  
 TYPE: PRT  
 ORGANISM: Enterococcus faecalis  
 US-09-134-000C-4868

Query Match 41.4%; Score 41; DB 4; Length 166;  
 Best Local Similarity 53.8%; Pred. No. 46;  
 Matches 7; Conservative 2; Mismatches 4;  
 QY 2 SDGLMNNNQTLFL 14  
 Db 86 SDRTWNNYBIF 98

RESULT 20

US-08-089-397A-11  
 Sequence 11, Application US/08089397A  
 Patent No. 6086880

GENERAL INFORMATION:  
 APPLICANT: FRENCHICK, PATRICK J.  
 APPLICANT: POTTER, ANDREW A.  
 APPLICANT: ILAZ, MOHAMMAD K.  
 APPLICANT: GILCHRIST, JAMES E.  
 APPLICANT: REDMOND, MARK J.

TITLE OF INVENTION: ROTAVIRUS VACCINES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER  
 STREET: 2000 Pennsylvania Avenue, NW  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/089,397A

FILING DATE: 07-JUL-1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: ADLER, REID G.

REGISTRATION NUMBER: 30,988

REFERENCE/DOCKET NUMBER: 29311-20003.03

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 326 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-089-397A-11

Query Match 41.4%; Score 41; DB 3; Length 326;  
 Best Local Similarity 57.1%; Pred. No. 98;  
 Matches 8; Conservative 1; Mismatches 5;  
 Indels 0; Gaps 0;

QY 2 SDGLMNNNQTLFL 15  
 Db 94 SDDEWENTISQFL 107

RESULT 21

5395759-2

Patent No. 5395759  
 APPLICANT: HOLMES, TAN H.; DYALL-SMITH, MICHAEL L.  
 TITLE OF INVENTION: DNA SEQUENCES AND AMINO ACID SEQUENCE  
 ENCODING THE HUMAN ROTAVIRUS MAJOR OUTER CAPSID GLYCOPROTEIN  
 NUMBER OF SEQUENCES: 14  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/474,642  
 FILING DATE: 29-APR-1985  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 834,704  
 FILING DATE: 04-FEB-1987

SEQ ID NO: 2;  
 LENGTH: 326

Query Match 41.4%; Score 41; DB 6; Length 326;  
 Best Local Similarity 57.1%; Pred. No. 98;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 SDGLMNNNQTLFL 15  
 Db 94 SDDEWENTISQFL 107

RESULT 22

US-09-248-796A-18622

Sequence 18622, Application US/09248796A

Patient No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO: 18622

LENGTH: 365

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-18622

Query Match 41.4%; Score 41; DB 4; Length 365;

Best Local Similarity 53.8%; Pred. No. 1.1e-02; Mismatches 5; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 GLWMNNNQTLFL 16  
 Db 279 GLWMNTATDFNIE 291

RESULT 23

US-09-248-796A-17089

Sequence 17089, Application US/09248796A

Patient No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO: 17089

LENGTH: 817

TYPE: PRT  
 ORGANISM: Candida albicans  
 US-09-248-796A-17089

Query Match 41.4%; Score 41; DB 4; Length 817;  
 Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSDGIWNNNOTQLF 14  
 Db 327 SIDKLUWNNDPQQYIF 340

RESULT 24  
 US-08-840-062-5  
 Sequence 5, Application US/08840062  
 Patent No. 6117977  
 GENERAL INFORMATION:  
 APPLICANT: LASKY, LAURENCE A.  
 TITLE OF INVENTION: TYPE C LECTINS  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (Genentech)  
 APPLICATION NUMBER: US/08/840,062  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Ginger R.  
 REGISTRATION NUMBER: 33,055  
 REFERENCE/DOCKET NUMBER: P1019R1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-3216  
 TELEFAX: 415/932-9881  
 TELEX: 9101371-7168  
 INFORMATION FOR SEQ ID NO: 5:  
 LENGTH: 1455 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-840-062-5

Query Match 41.4%; Score 41; DB 3; Length 1455;  
 Best Local Similarity 87.5%; Pred. No. 5.2e+02; Mismatches 7; Indels 0; Gaps 0;

QY 1 SSDGIWNN 8  
 Db 1335 SSSGIWNN 1342

RESULT 25  
 US-08-231-193A-11  
 Sequence 11, Application US/08231193A  
 General Information:  
 APPLICANT: Daggett, Lorrie P.  
 APPLICANT: Ellis, Steven B.  
 APPLICANT: Liaw, Chen W.  
 APPLICANT: Lu, Chin-Chun  
 TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA  
 NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/486,273A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/231,193  
 FILING DATE: 20-APR-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie  
 REFERENCE DOCKET NUMBER: 33,779  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-238-0899  
 TELEFAX: 619-238-0062  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 TYPE: amino acid  
 US-08-416-273A-11

RESULT 27  
 US-08-940-086A-11  
 Sequence 11, Application US/08940086A  
 Patent No. 6111091  
 GENERAL INFORMATION:  
 APPLICANT: Daggett, Lorrie P.  
 APPLICANT: Ellis, Steven B.  
 APPLICANT: Liaw, Chen W.  
 APPLICANT: Lu, Chin-Chun  
 TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
 TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
 NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Heller, Ehman White & McAuliffe  
 STREET: 4250 Executive Square, 7th Floor  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/436,332B  
 FILING DATE: 10-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YABLONSKY, MICHAEL D.  
 REGISTRATION NUMBER: 40,407  
 REFERENCE/DOCKET NUMBER: T1210Y  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 732-594-4678  
 TELEFAX: 732-594-4720  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: UNKNOWN  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-436-332B-10

RESULT 28  
 US-08-436-332B-10  
 Sequence 10, Application US/08436332B  
 Patent No. 6130058  
 GENERAL INFORMATION:  
 APPLICANT: LE COURDELLERES, BEATRICE  
 APPLICANT: MYERS, BEATRICE  
 APPLICANT: WHITING, PAUL JOHN  
 TITLE OF INVENTION: STABLY TRANSFECTED CELL LINE EXPRESSING  
 TITLE OF INVENTION: NMDA RECEPTORS, AND NOVEL CLONED NMDA  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.  
 STREET: 126 EAST LINCOLN AVE., - P.O. BOX 2000  
 CITY: Rahway  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07065  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/436,332B  
 FILING DATE: 10-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YABLONSKY, MICHAEL D.  
 REGISTRATION NUMBER: 40,407  
 REFERENCE/DOCKET NUMBER: T1210Y  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 732-594-4678  
 TELEFAX: 732-594-4720  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: UNKNOWN  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-436-332B-11

RESULT 29  
 US-08-940-035A-11  
 Sequence 11, Application US/08940035A  
 Patent No. 631661  
 GENERAL INFORMATION:  
 APPLICANT: Daggett, Lorrie P.  
 APPLICANT: Ellis, Steven B.

CURRENT APPLICATION DATA:  
 APPLICANT: Liaw, Chen W.  
 TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
 NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Heller Ehman White & McAuliffe  
 STREET: 4250 Executive Square, 7th Floor  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92037

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/940,035A  
 FILING DATE: 29-SEPT-97  
 PRIORITY APPLICATION DATA:  
 PRIORITY APPLICATION NUMBER: US 08/231,193  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie  
 REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-9383E  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-238-0999  
 TELEFAX: 619-238-0062

APPLICATION NUMBER: US 08/231,193  
 FILING DATE: 20-APR-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/052,449  
 FILING DATE: 20-APR-1993  
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie  
 REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-9383E  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-238-0999  
 TELEFAX: 619-238-0062

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/052,449  
 FILING DATE: 20-APR-1993  
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie  
 REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-9383E  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-238-0999  
 TELEFAX: 619-238-0062

INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-940-035A-11

RESULT 30  
 US-08-935-105A-11

Query Match Score 41; DB 3; Length 1464;  
 Best Local Similarity 41.4%; Pred. No. 5,3e+02;  
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY : :|||:||:||:||:  
 Db 1174 NEEGLSNNDQYKLYSKH 1190

RESULT 31  
 US-09-643-797-11

Query Match Score 41; DB 3; Length 1464;  
 Sequence 11, Application US/09648797  
 Best Local Similarity 41.2%; Pred. No. 5,3e+02;  
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY : :|||:||:||:||:  
 Db 1174 NEEGLSNNDQYKLYSKH 1190

Lu, Chin-Chun  
 TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
 NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Heller Ehman White & McAuliffe  
 STREET: 4250 Executive Square, 7th Floor  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/648,797  
 FILING DATE: 28-Aug-2000

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/940,086A  
 FILING DATE: 29-SEPT-97  
 APPLICATION NUMBER: US 08/231,193  
 FILING DATE: 20-APR-1994  
 APPLICATION NUMBER: US 08/052,449  
 FILING DATE: 20-APR-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 24735-9383C  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 450-8400  
 TELEFAX: (619) 450-8499  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TOPOLGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
 US-09-648-797-11

Query Match 41.4%; Score 41; DB 4; Length 1464;  
 Best Local Similarity 41.2%; Pred. No. 5.3e+02;  
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 SSDGWNNTQQLFLEH 17  
 Db 1174 NEEGLSNNDQKLYSKH 1190

RESULT 32  
 US-08-217-704C-2  
 ; Sequence 2, Application US/08217-704C  
 ; GENERAL INFORMATION:  
 ; Patent No. 6489124  
 ; APPLICANT: Folders, Robert  
 ; Fantaske, Robert  
 ; Adams, Sally-Lynn  
 ; Kamboj, Rajender  
 ; TITLE OF INVENTION: MODULATORY PROTEINS OF HUMAN CNS  
 ; RECEPIORS  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: Suite 500, 3000 K Street  
 ; CITY: Washington, D.C., N.W.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patientin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 PRIORITY APPLICATION DATA:  
 APPLICANT NUMBER: US 07/987, 953  
 FILING DATE: 25-Mar-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bent, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 16777/259/ALLE  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TOPOLGY: linear  
 MOLECULE TYPE: protein  
 ; US-09-386-123-11

RESULT 33  
 US-09-386-123-11  
 ; Sequence 11, Application US/09386123  
 ; GENERAL INFORMATION:  
 ; Patent No. 6521413  
 ; APPLICANT: Daggett, Lorrie P.  
 ; APPLICANT: Ellis, Steven B.  
 ; APPLICANT: Liaw, Chen W.  
 ; APPLICANT: Lu, Chin-Chun  
 ; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
 ; NUMBER OF SEQUENCES: 63  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Heller Ehrman White & McAuliffe  
 ; STREET: 4250 Executive Square, 7th Floor  
 ; CITY: La Jolla, CA  
 ; STATE: CA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patientin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 PRIORITY APPLICATION DATA:  
 APPLICANT NUMBER: US/09/386, 123  
 FILING DATE: 20-APR-1994  
 PRIOR APPLICATION DATA:  
 APPLICANT NUMBER: US 08/052, 449  
 FILING DATE: 20-APR-1993  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-9383F  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 858-450-8403  
 TELEX: 858-587-5360  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TOPOLGY: linear  
 MOLECULE TYPE: protein  
 ; US-09-386-123-11

RESULT 34  
 US-09-187-049-8  
 ; Sequence 8, Application US/09187049  
 ; General Information:  
 ; Patent No. 631766  
 ; APPLICANT: Lampka, Gayle K.  
 ; TITLE OF INVENTION: PLASTID PROTEOLYTIC PROCESSING ENZYME  
 ; TITLE OF INVENTION: THAT CLEAVES PRECURSOR POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: BRINKS HOFER GILSON & LIONE
; STREET: P.O. Box 10395
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610

; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,049
; FILING DATE: 2000-03-24
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/695,177
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin, Alice O.
; REGISTRATION NUMBER: 35,601
; REFERENCE/DOCKET NUMBER: 7814/16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312 321-4200
; TELEFAX: 312 321-4299
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: MPP B subunit from rat
; US-09-187-049-8

RESULT 35
; Best Local Similarity 40.4%; Score 40; DB 3; Length 124;
; Matches 10; Conservative 0; Mismatches 4; Indels 10; Gaps 1;
Qy 4 GLW-----NNNQTOFLEH 17
Db 20 GLWIDAGSRYENENKONGTAHFLEH 43

; US-09-540-236-3527
; Sequence 3527, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 16186
; LENGTH: 186
; TYPE: PRT
; ORGANISM: M.catarrhalis
; US-09-540-236-3527

RESULT 36
; Best Local Similarity 40.4%; Score 40; DB 4; Length 126;
; Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 3 DGLWMNNQTOFLEHS 18
Db 95 DGVVITNTGDDQFVEHS 110

; US-09-540-236-3527
; Query Match 40.4%; Score 40; DB 4; Length 126;
; Best Local Similarity 43.8%; Pred. No. 48; Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
; TYPE: PRT
; ORGANISM: M.catarrhalis
; US-09-540-236-3527

RESULT 37
; Best Local Similarity 40.4%; Score 40; DB 4; Length 141;
; Matches 10; Conservative 0; Mismatches 4; Indels 10; Gaps 1;
Qy 4 GLW-----NNNQTOFLEH 17
Db 82 GLWIDAGSRYENENKONGTAHFLEH 105

; US-09-248-796A-16186
; Sequence 16186, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16186
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-16186

RESULT 38
; Best Local Similarity 40.4%; Score 40; DB 4; Length 186;
; Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 3 DGLWMNNQTOFLEH 14
Db 34 DGLTMNSTQDQLF 45

; US-08-807-263-4
; Sequence 4, Application US/08007263C
; Patent No. 5985027
; GENERAL INFORMATION:
; APPLICANT: Mortensen, Uffe
; APPLICANT: Olesen, Kjeld
; APPLICANT: Steinicke, Henning
; APPLICANT: Sorensen, Steen B.
; APPLICANT: Breedam, Klaus
; TITLE OF INVENTION: MODIFIED CARBOXYPEPTIDASE

```

FILE REFERENCE: 8648.7ius01-no4  
; CURRENT APPLICATION NUMBER: US/08/807,263C  
; CURRENT FILING DATE: 1997-02-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 4  
; LENGTH: 421  
; TYPE: PRT  
; ORGANISM: *Saccharomyces cerevisiae*  
; US-08-807-263-4

Query Match 40.4%; Score 40; DB 2; Length 421;  
Best Local Similarity 54.5%; Pred. No. 1.9e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 WNNNOTQFLE 16  
Db 84 WNSNATVIED 94

RESULT 39 Application US/09375140

; Sequence 10, Application US/09375140

; PATENT NO. 6489540

; GENERAL INFORMATION:

; APPLICANT: Kavanagh, T.

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; PRIORITY APPLICATION NUMBER: PP-0343 US

; APPLICATION NUMBER:

; FILING DATE:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEGRAM:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 489 amino acids

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; IMMEDIATE SOURCE:

; LIBRARY: BRAINOT14

; CLONE: 1533490

; US-08-895-521-1

Query Match 40.4%; Score 40; DB 2; Length 489;

Best Local Similarity 42.9%; Pred. No. 2.1e+02;

Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

RESULT 40 Application US/08-895-521-1

; Sequence 1, Application US/08895521

; GENERAL INFORMATION:

; PATENT NO. 5869311

; APPLICANT: Bandman, Olga

; ATTORNEY/AGENT INFORMATION:

; NAME: Shah, Purvi

; REGISTRATION NUMBER: 36,749

; PRIORITY APPLICATION NUMBER: PP-0343 US

; APPLICATION NUMBER:

; FILING DATE:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEGRAM:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 489 amino acids

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; IMMEDIATE SOURCE:

; LIBRARY: BRAINOT14

; CLONE: 1533490

; US-08-895-521-1

Query Match 40.4%; Score 40; DB 2; Length 489;

Best Local Similarity 41.7%; Pred. No. 2.2e+02;

Matches 10; Conservative 0; Mismatches 4; Indels 10; Gaps 1;

Search completed: December 30, 2004, 16:14:38  
Job time : 40 secs

*This Page Blank (uspto)*

Result No.	Score	Query Match length	DB ID	Description
1	99	100.0	359	043656 homo sapien
2	99	100.0	364	096442 homo sapien
3	99	100.0	364	CAG33395 homo sapien
4	84	84.8	451	095144 cercopithecus aethiops
5	84	84.8	460	018984 cercopithecus aethiops
6	84	84.8	469	07TJ48 cercopithecus aethiops
7	84	84.8	473	Q7JJ47 cercopithecus aethiops
8	84	84.8	474	046597 cercopithecus aethiops
9	84	84.8	478	046598 cercopithecus aethiops
10	51	51.5	392	1 CEMMA_NEPOL nephrosemili
11	49	49.5	267	2 Q8ZS98 anabaena sp
12	49	49.5	278	1 CEMA_GUTHI pseudomonas
13	49	49.5	338	P73105 synchocystis
14	48	48.5	129	2 Q8BRW1 obryon
15	48	48.5	416	1 HAPC_PIG sus scrofa
16	48	48.5	558	2 O36293 venezuelan
17	48	48.5	558	2 O36294 venezuelan
18	48	48.5	559	2 O9WC99 venezuelan
19	48	48.5	559	2 O36298 venezuelan
20	48	48.5	559	2 O36308 venezuelan
21	48	48.5	559	2 O36309 venezuelan
22	48	48.5	559	2 O41997 venezuelan
23	48	48.5	559	2 O9WC99 venezuelan
24	48	48.5	559	2 O9WC99 venezuelan
25	48	48.5	559	2 O98755 venezuelan
26	48	48.5	559	2 Q8V5J7 venezuelan
27	48	48.5	559	2 Q8V5J8 venezuelan
28	48	48.5	1254	1 POLS_BEVNB polystomidae
29	48	48.5	1254	1 POLS_BEVVE polystomidae
30	48	48.5	1254	1 POLS_BEVVT polystomidae
31	48	48.5	1254	1 Q77VY8 venezuelan

OM protein - protein search, using sw model  
Run on: December 30, 2004, 16:03:35 ; Search time 190 Seconds  
( without alignments)  
54.509 Million cell updates/sec

Title: US-10-718-321-1  
Perfect score: 99  
Sequence: 1 SSDGLWNWNQNQTQLFLEHS 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 57537466 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
listing first 150 summaries

Database : UniProt\_02:  
1: uniprot\_sprot:  
2: uniprot\_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	99	100.0	359	2 043656 homo sapien
2	99	100.0	364	2 096442 homo sapien
3	99	100.0	364	CAG33395 homo sapien
4	84	84.8	451	2 095144 cercopithecus aethiops
5	84	84.8	460	2 018984 cercopithecus aethiops
6	84	84.8	469	2 07TJ48 cercopithecus aethiops
7	84	84.8	473	2 Q7JJ47 cercopithecus aethiops
8	84	84.8	474	2 046597 cercopithecus aethiops
9	84	84.8	478	2 046598 cercopithecus aethiops
10	51	51.5	392	1 CEMMA_NEPOL nephrosemili
11	49	49.5	267	2 Q8ZS98 anabaena sp
12	49	49.5	278	1 CEMA_GUTHI pseudomonas
13	49	49.5	338	2 P73105 synchocystis
14	48	48.5	129	2 Q8BRW1 obryon
15	48	48.5	416	1 HAPC_PIG sus scrofa
16	48	48.5	558	2 O36293 venezuelan
17	48	48.5	558	2 O36294 venezuelan
18	48	48.5	559	2 O9WC99 venezuelan
19	48	48.5	559	2 O36298 venezuelan
20	48	48.5	559	2 O36308 venezuelan
21	48	48.5	559	2 O36309 venezuelan
22	48	48.5	559	2 O41997 venezuelan
23	48	48.5	559	2 O9WC99 venezuelan
24	48	48.5	559	2 O9WC99 venezuelan
25	48	48.5	559	2 Q98755 venezuelan
26	48	48.5	559	2 Q8V5J7 venezuelan
27	48	48.5	559	2 Q8V5J8 venezuelan
28	48	48.5	1254	1 POLS_BEVNB polystomidae
29	48	48.5	1254	1 POLS_BEVVE polystomidae
30	48	48.5	1254	1 POLS_BEVVT polystomidae
31	48	48.5	1254	1 Q77VY8 venezuelan

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

Q9YKCA venezuelan  
Aadi4551 venezuelan  
P36329 venezuelan  
P36332 venezuelan  
036387 venezuelan  
036388 venezuelan  
036300 venezuelan  
090164 venezuelan  
091628 venezuelan  
061593 venezuelan  
061595 venezuelan  
094cf4 venezuelan  
094cf5 venezuelan  
094cf7 venezuelan  
094cf8 venezuelan  
094cf9 venezuelan  
094cf10 venezuelan  
094cf11 arabidopsis  
06cu80 kluveromyces  
07yrd94 echinops te  
093285 echinops te  
06cb54 yarrowia li  
09wn27 venezuelan  
09t011 solanum tub  
06cu80 kluveromyces  
07yrd20 human immun  
075021 human immun  
075022 human rotav  
P08290 rattus norv  
Q9nwgb homo sapien  
Q6uxw4 homo sapien  
Q9xcl8 bacteroides  
Q88tk4 pseudomonas  
Q6f1h3 candida gla  
P34336 mus musculus  
Q05959 oryza sativ  
Q9c5x5 arabidopsis  
Q9hm55 homo sapien  
Q9m977 streptomyce  
P38109 saccharomyces  
Q94au9 solanum tub  
Q8159 oryza sativ  
Q9c5x5 arabidopsis  
Baa01069 mus muscu  
Q9m89 rhizobium m  
Q9kel1 candida gla  
Q75012 human immun  
Q75014 human immun  
Q75015 human immun  
Q9mmt7 mesostigma  
Q81515 meristigma  
Q72n84 leptospira  
Q8ffcc3 leptospira  
Aa871503 leptospira  
Q7vok4 bandicota  
Q6j3z8 bartonella  
Q6164 bartonella  
Q827j3 enterococcus  
Q8w108 psilotum nu  
Q72v11 desulfobacter  
Aa89496 desulfobacter  
Q6ccv9 yarrowia li  
Q77j1 ashbya goss  
Aa852706 ashbya go  
Q7rxw8 neurospora  
Q96fc99 homo sapien  
Q61949 homo sapien  
Bad19019 homo sapi  
Q9ew23 mus musculus  
P08483 rattus norv



DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 364 AA; 39249 MW; AA67CTDC7FAC81F1 CRC64;  
 Query Match 100.0%; Score 99; DB 2; Length 364;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNNOTQLEHHS 18  
 Db 269 SSDGLWNNNOTQLEHHS 286

RESULT 3  
 CAG33395 PRELIMINARY; PRT; 364 AA.  
 ID CAG33395  
 AC CAG33395;  
 DT 01-JUN-2004 (TREMBrel. 27, Created)  
 DT 01-JUN-2004 (TREMBrel. 27, Last sequence update)  
 DE HAVER1 protein.  
 GN HAVER1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TAXID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ebert L., Schick M., Neubert P., Schatzen R., Henze S., Korn B.;  
 RT "Cloning of human full open reading frames in Gateway™ system entry  
 vector (pDON201);"  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CIG45714; CAG33395.1; -.  
 SQ SEQUENCE 364 AA; 39249 MW; AA67CTDC7FAC81F1 CRC64;

Query Match 100.0%; Score 99; DB 2; Length 364;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNNOTQLEHHS 18  
 Db 269 SSDGLWNNNOTQLEHHS 286

RESULT 4  
 Q93144 PRELIMINARY; PRT; 451 AA.  
 ID Q93144  
 AC Q93144;  
 DT 01-FEB-1997 (TREMBrel. 02, Created)  
 DT 01-FEB-1997 (TREMBrel. 02, Last sequence update)  
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)  
 DE HAVER1 protein precursor.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TAXID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.

Query Match 84.8%; Score 84; DB 2; Length 451;  
 Best Local Similarity 88.9%; Pred. No. 9.5e-05;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNNOTQLEHHS 18  
 Db 353 SSDGLWNNNOTQLEHHS 370

RESULT 5  
 OI18984 PRELIMINARY; PRT; 460 AA.  
 ID OI18984  
 AC OI18984;  
 DT 01-JAN-1998 (TREMBrel. 05, Created)  
 DT 01-JAN-1998 (TREMBrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)  
 DE Hepatitis A virus receptor.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OX NCBI\_TAXID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=97368416; PubMed=9225030;  
 RA Ashida M., Hamada C.;  
 RT "Molecular cloning of the hepatitis A virus receptor from a simian  
 cell line.";  
 RL J. Gen. Virol. 78:1565-1569(1997).  
 DR EMBL; DB88585; BA21556.1; -.  
 DR GO; GO:0004872; Receptor activity; IEA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR07110; Ig-like.  
 DR InterPro; IPR03006; Ig\_MHC.  
 DR SMART; SM00405; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE 460 AA; 49887 MW; IDIA0C1D832139EA CRC64;

Query Match 84.8%; Score 84; DB 2; Length 460;  
 Best Local Similarity 88.9%; Pred. No. 9.7e-05;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNNOTQLEHHS 18  
 Db 353 SSDGLWNNNOTQLEHHS 370

RESULT 6  
 O77048 PRELIMINARY; PRT; 469 AA.  
 ID O77048  
 AC O77048;  
 DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DE Hepatitis A virus cellular receptor 1 short form.  
 GN Name=HAVER-1;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TAXID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=88285791; PubMed=9621093;  
 RA Feigelson D., Thompson P., Mattoo P., Kaplan G.G.;

RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African green monkey kidney cells result in antigenic variants that do not react with protective monoclonal antibody 190/4.";  
 RT J. Virol. 72:6218-6222(1998).  
 RL EMBL; ARF43446; AAC3971.1; -. DR GO; GO:0004872; F-receptor activity; IEA.  
 DR InterPro; IPR03599; IG-like.  
 DR IPR00110; IG-like.  
 DR InterPro; IPR00306; IG\_MHC.  
 DR SMART; SMO409; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE: 469 AA; 50561 MW; 278386F47948F528 CRC64;

Query Match 84.8%; Score 84; DB 2; Length 469;  
 Best Local Similarity 88.9%; Pred. No. 9.9e-05; 0; Mismatches 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQTLFLEHS 18  
 Db 362 SSDGLWNNTQTLFLEHS 379

RESULT 7

ID Q7UJ47 PRELIMINARY; PRT; 473 AA.  
 AC Q7UJ47; RPP  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hepatitis A virus cellular receptor 1 short form.  
 GN Name=HAVER-1;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98285791; PubMed=9621093;  
 RA Feigelson D., Thompson P., Mattoo P., Kaplan G.G.;  
 RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African green monkey kidney cells result in antigenic variants that do not react with protective monoclonal antibody 190/4.";  
 RT J. Virol. 72:6218-6222(1998).  
 DR EMBL; ARF43448; AAC3973.1; -. DR GO; GO:0004872; F-receptor activity; IEA.  
 DR InterPro; IPR03599; IG-like.  
 DR InterPro; IPR00110; IG-like.  
 DR SMART; SMO409; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE: 474 AA; 51088 MW; 472DF87C9220524 CRC64;

Query Match 84.8%; Score 84; DB 2; Length 474;  
 Best Local Similarity 88.9%; Pred. No. 0.0001; 0; Mismatches 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQTLFLEHS 18  
 Db 367 SSDGLWNNTQTLFLEHS 384

RESULT 9

ID Q46598 PRELIMINARY; PRT; 478 AA.  
 AC Q46598; RPP  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DE Hepatitis A virus cellular receptor 1 long form.  
 GN Name=HAVER-1;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98285791; PubMed=9621093;  
 RA Feigelson D., Thompson P., Mattoo P., Kaplan G.G.;  
 RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African green monkey kidney cells result in antigenic variants that do not react with protective monoclonal antibody 190/4.";  
 RT J. Virol. 72:6218-6222(1998).  
 DR EMBL; ARF43449; AAC39774.1; -. DR GO; GO:0004872; F-receptor activity; IEA.  
 DR InterPro; IPR03599; IG-like.  
 DR InterPro; IPR00110; IG-like.  
 DR SMART; SMO409; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE: 478 AA; 51501 MW; 3A919655C752FF60 CRC64;

Query Match 84.8%; Score 84; DB 2; Length 478;  
 Best Local Similarity 88.9%; Pred. No. 0.0001; 0; Mismatches 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQTLFLEHS 18  
 Db 366 SSDGLWNNTQTLFLEHS 383

RESULT 8

ID Q46597 PRELIMINARY; PRT; 474 AA.  
 AC Q46597; RPP  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)



FT	TRANSMEM	239	259	Potential	DE enriched library, clone:A530092L01 product:hypothetical protein, full insert sequence;
SQ	SEQUENCE	278 AA;	32209 MW;	1E7881/DC25582DE CRC64;	DE insert sequence;
Query Match		49.5%	Score 49;	DB 1;	Mus musculus (Mouse).
Best Local Similarity		50.0%	Pred. No. 19;	Best Local Similarity 50.0%; Pred. No. 19;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Matches		8;	Conservative	3;	OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
RESULT 13					OX NCBI_TaxID=10090;
P73105	PRELIMINARY;		PRT;	338 AA.	RN [1];
ID P73105					RN SEQUENCE FROM N.A.
AC P73105;					RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;
DT 01-FEB-1997 (TREMBLrel. 02, Created)					RC MEDLINE=9279253; PubMed=10349636;
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)					RA Carninci P.; Hayashizaki Y.;
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)					RT "High-efficiency full-length cDNA cloning.";
DE N-acetyl-muramoyl-L-alanine amidase.					RL Mech. Enzymol. 303:19-44(1999).
GN Name=amidA; Order=eduSpeciesName=SIRI910;					RN [2];
OS Synechocystis sp. (strain PCC 6803);					RP SEQUENCE FROM N.A.
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.					RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
OX NCBI_TaxID=1148;					RA MEDLINE=2105660; PubMed=11217851;
RN [1]					RL Nature 409:685-690(2001).
RP SEQUENCE FROM N.A.					RN [3];
RX MEDLINE=96121529; PubMed=8590279;					RP SEQUENCE FROM N.A.
RA Kameko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Suguri M., Tabata S., Watanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.", DNA Res. 2:153-166(1995).					RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RT DNA Res. 2:153-166(1995).					RA The RIKEN Consortium'
RL [2]					RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RN SEQUENCE FROM N.A.					RA "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RC STRAIN=PCC6803; MEDLINE=2049374; PubMed=11042159;					RL Nature 420:563-573(2002).
RX MEDLINE=97061201; PubMed=8905231;					RN [4];
RA Kameko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hiroswawa M., Suguri M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3:109-136(1996).					RP SEQUENCE FROM N.A.
RT DNA Res. 3:109-136(1996).					RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RL EMBL; DQ09103; BAA-7131.1; -.					RA Carninci P.; Shibata Y., Hayashizaki Y.;
DR EMBL; S75217; S75217.					RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.					RA "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.", RIKEN Genome Res. 10:1617-1630(2000).
DR GO; GO:0008745; P:N-acetylmuramoyl-L-alanine amidase activity; IEA.					RN [5];
DR InterPro; IPR002508; Amidase_3_beta-hydro.					RP SEQUENCE FROM N.A.
DR PFAM; PF01520; Amidase_3; 1.					RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
DR SMART; SM0646; Ami_3; 1.					RA MEDLINE=2050913; PubMed=11076861;
KW Compleat_Proteom.					RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Kitabayashi T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Wakihira M., Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsunaga S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y., RIKEN integrated sequencing pipeline with 304 multicapillary sequencer.,"; Genome Res. 10:1757-1771(2000).
RN [6];					RN [6];
RP SEQUENCE FROM N.A.					RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;					RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanada K., Hara A., Hachizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T., Horii F., Imotani K., Ishii Y., Itoh M., Kegawa I., Kasukawa T., Katoch H., Kawai J., Kohji Y., Kondo S., Kondo H., Kouda M., Koya S., Kuribara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ono M., Ohseto N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sobage Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., RIKEN submitted (JMI-2001) to the EMBL/Genbank/DDBJ databases.					
DR EMBL; AK041221; BAC30867.1; -.					RN [7];
KW Hypothetical protein.					RP SEQUENCE 129 AA; 14724 MW; A9D2912B74A4885 CRC64;
SQ SEQUENCE 129 AA; 14724 MW; A9D2912B74A4885 CRC64;					RA Query Match
Best Local Similarity 48.5%; Score 48;	DB 2;	Length 129;			RA Best Local Similarity 48.5%; Score 48;
Matches 9;	Conservative 2;	Mismatches 5;	Indels 0;	Gaps 0;	RA Matches 9;
RESULT 14					RA Conservative 2;
QB8RW1 PRELIMINARY;	PRT;	129 AA.			RA Mismatches 5;
ID QB8RW1; OC 01-MAR-2003 (TREMBLrel. 23, Created)					RA Indels 0;
DT 01-OCT-2003 (TREMBLrel. 23, Last sequence update)					RA Gaps 0;
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)					RA Submitted (JMI-2001) to the EMBL/Genbank/DDBJ databases.
DR Mus musculus adult male aorta and vein cDNA, RIKEN full-length					DR EMBL; AK041221; BAC30867.1; -.

QY 2 SDGLWNNTQTLPEH 17  
 52 SCGLWNPSPQTHLFIVH 67

RESULT 15

HAPC PIG STANDARD; PRT; 416 AA.

ID P17630; DT 01-AUG-1990 (Rel. 15, Created)  
 DE Haptocorbin precursor (R protein) (Cobalophilin) (Fragment).

DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.

OX NCBI\_TaxID=9823; RN [1]; RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-STOMACH; MEDLINE-90235848; PubMed=2331993; RT Hevitt J.E., Seetharam B., Leykam J.F., Alpers D.H.; CC --Isolation and characterization of a cDNA encoding porcine gastric RT haptocorbin."; Bur. J. Biomed. 189:125-130(1990).  
 CC -I- FUNCTION: May play a role in preventing the absorption of cobalamin analogs produced by bacteria. Binds to cobalamin and to cobalamin analogs such as cobinamide.

CC --I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- TISSUE SPECIFICITY: Haptocorrins are a family of cobalamin-binding glycoproteins found in blood, salivary and mucosal secretions.

CC -I- PTM: Contains about 30% carbohydrates.  
 CC -I- SIMILARITY: Belongs to the eukaryotic cobalamin transport proteins family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@ibb-sib.ch).

DR EMBL; X52566; CAA36800.1; -.

DR PIR; S09334; S09334.

DR InterPro; IPR002157; Cobalamin\_bind.

DR Pfam; PF01122; Cobalamin\_bind.

DR PROSITE; PS00468; COBALAMIN\_BINDING\_1.

KW Cobalt transport; Direct protein sequencing; Glycoprotein; Signal;

KW Transport.

FT NON\_TER 1 1 FT SIGNAL 25 416 FT CHAIN 25 416 FT DISULFID 155 197 FT CARBOHYD 89 89 FT CARBOHYD 160 160 FT CARBOHYD 165 165 FT CARBOHYD 178 178 FT CARBOHYD 311 311 FT CARBOHYD 327 327 FT CARBOHYD 344 344 FT CARBOHYD 359 359

PROBABLE. By similarity. N-linked (GlcNAc. . . ) (Potential). N-linked (GlcNAc. . . ) (Potential).

SEQUENCE 416 AA; 46963 MW; 3380CG6F4CB84AE3 CRC64;

Query Match 1 SDGLWNNTQTLPEH 16

QY 1 SDGLWNNTQTLPEHS 18

Db 378 SVQGIWANNRERTWHEHS 395

RESULT 16

O36293 PRELIMINARY; PRT; 558 AA.

ID O36293; AC O36293; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Polypeptide (Fragment)

OS Venezuelan equine encephalitis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus; VEEV complex.

OX NCBI\_TaxID=11036; RN [1]; RP SEQUENCE FROM N.A.

RC STRAIN=10T1724; MEDLINE-97404681; PubMed=9261393; RT Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M., Smith J.R., Kang W., Sweeney W.P., Weaver S.C.; CC "Repeated emergence of epidemic/epizootic Venezuelan equine encephalitis from a single genotype of enzootic subtype ID virus."; RL Virol. 71:669-76705(1997).

DR EMBL; AF004464; AAB81710.1; -.

DR GO: GO:0019031; C.viral capsid; IEA.

DR GO: GO:0019031; C.viral envelope; IEA.

DR GO: GO:005198; F.structural molecule activity; IEA.

DR InterPro; IPR002568 Alpha\_E1\_glycop.

DR InterPro; IPR003936; Alpha\_E2\_glycop.

DR InterPro; IPR002333; Alpha\_B3\_glycop.

DR InterPro; IPR00336; Flavi\_glycoprote.

DR Pfam; PF01587; Alpha\_E1\_glycop; 1.

DR Pfam; PR00943; Alpha\_E2\_glycop; 1.

DR Pfam; PR01563; Alpha\_E3\_glycop; 1.

KW Polyprotein.

FT NON\_TER 1 1 FT CHAIN 538 >558 FT NON\_TER 558 558

FT SEQUENCE 558 AA; 61777 MW; 82FCDD3D51D15729 CRC64;

Query Match 1 SDGLWNNTQTLPEH 16

QY 1 SDGLWNNTQTLPEHS 18

Db 487 SLDHWNNTQQMFIQ 502

RESULT 17

O36294 PRELIMINARY; PRT; 558 AA.

ID O36294; AC O36294; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Polypeptide (Fragment)

OS Venezuelan equine encephalitis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus; VEE complex.

OX NCBI\_TaxID=11036; RN [1]; RP SEQUENCE FROM N.A.

RC STRAIN=V209A; MEDLINE-97404681; PubMed=9261393; RT Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M., Smith J.F., Kang W., Sweeney W.P., Weaver S.C.; CC "Repeated emergence of epidemic/epizootic Venezuelan equine encephalitis from a single genotype of enzootic subtype ID virus."; RL Virol. 71:669-76705(1997).

DR EMBL; AF004465; AAB81711.1; -.

DR GO; GO:0019031; C.viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR02548; Alpha\_E1\_glycop.  
 DR InterPro; IPR00936; Alpha\_E2\_glycop.  
 DR InterPro; IPR02533; Alpha\_E3\_glycop.  
 DR InterPro; IPR00336; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.  
 FT NON\_TER 1 1 envelope glycoprotein E2.  
 FT CHAIN <1 537 envelope glycoprotein E1.  
 FT NON\_TER 538 558  
 SQ SEQUENCE 558 AA; 61626 MW; 95ED71BDDF81B5BC CRC64;  
 Query Match 48.5%; Score 48; DB 2; Length 558;  
 Best Local Similarity 50.0%; Pred. No. 60;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 SSDGLIMNNQ--TQFL 16  
 Db 487 SLDHLWNQQMWFQ 502  
 RESULT 18  
 ID 036297 PRELIMINARY; PRT; 559 AA.  
 ID 036297; AC 559 AA.  
 ID 036297; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 ID 036297; DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 ID 036297; DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Polyprotein (Fragment).  
 OS Venezuelan equine encephalitis virus.  
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 NCBI\_TaxID=11036;  
 RN [1] SEQUENCE FROM N.A.  
 RP STRAIN=Fes-47et;  
 RC MEDLINE=97404681; PubMed=9261393;  
 RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M.,  
 RA Smith J.F., Kang W., Sweeney W.P., Weaver S.C.;  
 RT "Repeated emergence of epidemic/epizootic Venezuelan equine  
 encephalitis from a single genotype of enzootic subtype ID virus.";  
 RL J. Virol. 71:6697-6705(1997).  
 DR EMBL; AF004468; AAB81713; 1.  
 DR GO; GO:019028; C:viral capsid; IEA.  
 DR GO; GO:019031; C:viral envelope; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR00936; Alpha\_E1\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR InterPro; IPR000336; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E2\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.  
 FT NON\_TER 1 1 envelope glycoprotein E2.  
 FT CHAIN <1 537 envelope glycoprotein E1.  
 FT NON\_TER 538 559  
 SQ SEQUENCE 559 AA; 61749 MW; 93A484BFCAA29217P CRC64;  
 Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 57.9%; Pred. No. 61;  
 Matches 11; Conservative 1; Mismatches 3; Indels 4; Gaps 0;  
 Qy 1 SSDGLIMNNQ--TQFL 15  
 Db 487 SLDHLWNQQMWFQ 505  
 RESULT 20  
 ID 036308 PRELIMINARY; PRT; 559 AA.  
 ID 036308; AC 559 AA.  
 ID 036308; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 ID 036308; DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 ID 036308; DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Polyprotein (Fragment).  
 OS Venezuelan equine encephalitis virus.  
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 NCBI\_TaxID=11036;  
 RN [1] SEQUENCE FROM N.A.  
 RP STRAIN=DE15191;  
 RC MEDLINE=97404681; PubMed=9261393;  
 RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M.,  
 RA Smith J.F., Kang W., Sweeney W.P., Weaver S.C.;  
 RT "Repeated emergence of epidemic/epizootic Venezuelan equine  
 encephalitis from a single genotype of enzootic subtype ID virus.";  
 RL J. Virol. 71:6697-6705(1997).  
 DR EMBL; AF004852; AAB81715; 1.  
 DR GO; GO:019028; C:viral capsid; IEA.  
 DR GO; GO:019031; C:viral envelope; IEA.  
 DR GO; GO:005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR002548; Alpha\_E1\_glycop.

DR InterPro; IPR000936; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.  
 FT NON TER 1 1 envelope glycoprotein E2.  
 FT CHAIN <1 537 envelope glycoprotein E1.  
 FT CHAIN 538 >559  
 FT NON TER 559 559 MW: AF95819323F72337 CRC64;  
 SQ SEQUENCE 559 AA; 61784 MW;  
 Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 OQ 1 SSDGLWNNNNOTQLELE 16  
 Db 487 SLDHLWNNNQQMFWMQ 502

RESULT 21

ID 036309 PRELIMINARY; PRT; 559 AA.

AC 036309; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DB Polyprotein (fragment).

OS Venezuelan equine encephalitis virus.  
 OS Venezuelan equine encephalitis virus, no DNA stage; Togaviridae;  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 RT "Re-emergence of epidemic Venezuelan equine encephalomyelitis in South America. VEE Study Group.";  
 RL Lancet 348:436-440(1996).  
 RN [2]  
 RP STRAIN=Panaquire;  
 RA Weaver S.C.;  
 RL Submitted (SBR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U55346; AAC2613.1;  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR InterPro; IPR02548; Alpha\_E1\_glycop.  
 DR InterPro; IPR002533; Alpha\_E2\_glycop.  
 DR InterPro; IPR000936; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.  
 FT NON TER 1 1 protein E2.  
 FT CHAIN <1 537 protein E1.  
 FT NON TER 538 >559  
 SQ SEQUENCE 559 AA; 61754 MW; C48D0AF23677E6A0 CRC64;

Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 OQ 1 SSDGLWNNNNOTQLELE 16  
 Db 487 SLDHLWNNNQQMFWMQ 502

RESULT 23

ID Q9WCF9 PRELIMINARY; PRT; 559 AA.

AC Q9WCF9; DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DB Structural polyprotein (Fragment).

OS Venezuelan equine encephalitis virus.  
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 OC NCBI\_TaxID=11036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Pura;  
 RA Weaver S.C.; Pfeiffer M.; Marriott K.; Kang W.; Kinney R.M.;  
 RT "Genetic evidence for the origins of Venezuelan equine encephalitis virus subtype TAB outbreaks"; Am. J. Trop. Med. Hyg. 60:441-448 (1999).  
 DR EMBL; AF093104; AAD37003.1;  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.

RESULT 22

ID 041997 PRELIMINARY; PRT; 559 AA.

Db 487 SLDHLWNNNQQMFWMQ 502

RESULT 23

ID Q9WCF9 PRELIMINARY; PRT; 559 AA.

AC 041997; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DB Structural polyprotein (Fragment).

OS Venezuelan equine encephalitis virus.  
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 OC NCBI\_TaxID=11036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Pura;  
 RA Weaver S.C.; Pfeiffer M.; Marriott K.; Kang W.; Kinney R.M.;  
 RT "Genetic evidence for the origins of Venezuelan equine encephalitis virus subtype TAB outbreaks"; Am. J. Trop. Med. Hyg. 60:441-448 (1999).  
 DR EMBL; AF093104; AAD37003.1;  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F-structural molecule activity; IEA.  
 DR InterPro; IPR002548; Alpha\_E2\_glycop.  
 DR InterPro; IPR00936; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR InterPro; IPR000336; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.

FT NON TER 559 559  
 SQ SEQUENCE 559 AA; 520:5 MW; 6646981:CG6BB1:7B50 CRC64;  
 Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 487 SLDHLWNQNNQMFNWIQ 502

RESULT 24  
 Q9WCG0 PRELIMINARY; PRT; 559 AA.  
 ID Q9WCG0;  
 AC 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Structural polyprotein (Fragment).  
 OS Venezuelan equine encephalitis virus.  
 RT viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 RN [1] \_TAXID=11036;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E123/69;  
 RX MEDLINE:99394886; PubMed=10466974;  
 RA Weaver S.C., Preffer M., Marriott K., Kang W., Kinney R.M.;  
 RT "Genetic evidence for the origins of Venezuelan equine encephalitis  
 virus subtype LAB outbreaks";  
 RL Am. J. Trop. Med. Hyg. 60:441-448(1999).

DR EMBL; AR093105; Aad370041; -.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F-structural molecule activity; IEA.  
 DR InterPro; IPR002548; Alpha\_E1\_glycop.  
 DR InterPro; IPR00936; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR InterPro; IPR000336; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.

FT NON TER 559 559  
 SQ SEQUENCE 559 AA; 61820 MW; E03AD37D4AB6AB54 CRC64;  
 Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 487 SLDHLWNQNNQMFNWIQ 502

RESULT 25  
 Q98755 PRELIMINARY; PRT; 559 AA.  
 ID Q98755  
 AC 098755;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)

Query Match 1 SDGGLWNQNTQLQFLE 16  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 487 SLDHLWNQNNQMFNWIQ 502

RESULT 26  
 Q8V5J7 PRELIMINARY; PRT; 559 AA.  
 ID Q8V5J7;  
 AC 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Structural polyprotein (Fragment).  
 OS Venezuelan equine encephalitis virus.  
 RT viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 RN [1] \_TAXID=11036;  
 RP SEQUENCE FROM N.A.  
 RA Weaver S.C., Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; ARF48316; Aml57189.1; -.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F-structural molecule activity; IEA.  
 DR InterPro; IPR002548; Alpha\_E1\_glycop.  
 DR InterPro; IPR00936; Alpha\_E2\_glycop.  
 DR InterPro; IPR000336; Alpha\_E3\_glycop.  
 DR InterPro; IPR002533; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.

FT NON TER 559 559  
 SQ SEQUENCE 559 AA; 61823 MW; 9D14BF8740780862 CRC64;



OX NCBI\_TaxID=34383;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93187617; PubMed=8445371;  
 RA "Molecular evidence that epizootic Venezuelan equine encephalitis  
 RT (VERB) I-AB viruses are not evolutionary derivatives of enzootic VEE  
 RT subtype I-E or II viruses.";  
 RL J. Gen. Virol. 74:1519-523 (1993).  
 CC -- FUNCTION: The capsid protein is an auto-protease.  
 CC -- PTM: Specific enzymatic cleavages in vivo yield mature proteins.  
 CC -- MISCELLANEOUS: The 6 kDa polypeptide probably serves as the signal  
 sequence for the membrane glycoprotein El, which is the viral  
 hemagglutinin.

-- SIMILARITY: The protease belongs to peptidase family S3.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 or send an email to license@isb-sib.ch).

CC

CC

CC DR EMBL; LO4598; AAA42984\_1; --  
 DR EMBL; LO4598; AAA42983\_1; ALT TERM.  
 DR EMBL; LO4598; AAA42985\_1; ALT SEQ.  
 DR EMBL; LO4598; AAA42986\_1; ALT SEQ.  
 DR EMBL; LO4598; AAA42987\_1; ALT SEQ.  
 DR EMBL; LO4598; AAA42988\_1; ALT INIT.  
 DR PIR; JO1978; JO1978.  
 DR HSSP; P05674; IEP5.  
 DR MEROPS; S03\_001; --  
 DR InterPro; IPR002548; Alpha\_E1\_glycop.  
 DR InterPro; IPR002546; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Flavi\_glycoprote.  
 DR InterPro; IPR000336; Peptidase\_S3.  
 DR InterPro; IPR000903; Pept\_Ser\_Cys.  
 DR Pfam; PF00944; Alpha\_core; 1.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
 DR PRINTS; PR00798; TOGAIRIN.  
 DR KW Coat protein; Glycoprotein; Hydrolase; Polyprotein; Serine protease;  
 KW Transmembrane.

FT CHAIN 1 274 Coat protein C.  
 FT CHAIN 275 333 Spike glycoprotein B3.  
 FT CHAIN 334 756 Spike glycoprotein B2.  
 FT CHAIN 757 813 6 kDa peptide.

FT ACT SITE 1254 151 Spike glycoprotein El.

FT ACT SITE 157 157 Charge relay system (By similarity).  
 FT ACT SITE 225 225 Charge relay system (By similarity).  
 FT TRANSMEM 701 721 Charge relay system (By similarity).  
 FT TRANSMEM 794 813 Potential.

FT TRANSMEM 1231 1248 Potential.

FT CARBOHYD 47 47 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 285 285 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 545 545 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 651 651 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 946 946 N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 1254 AA: 138337 MW: 293DEP37F9B92C4B CRC64;

Query Match 48 5%; Score 48; DB 1; Length 1254;  
 Best local Similarity 57.9%; Fred. No. 1.5e+02; Mismatches 3; Indels 4; Gaps 1;  
 Matches 11; Conservative 1; MisMatches 3; Indels 4; Gaps 1;

Qy 1 SDGJGMNNO---TQFL 15  
 Qy 762 SLDHWNWNQCMFWIQLLI 780

RESULT 30  
 POIS\_BEVTT STANDARD; PRNT; 1254 AA.  
 ID POIS\_BEVTT  
 AC P0592; Q88691; Q88692; Q88693; Q88694; Q88695;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Structural polypeptide (P10) [Contains: Coat protein C (EC 3.4.21.-)  
 DE (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2; 6  
 kDa peptide; Spike glycoprotein El].  
 OS Venezuelan equine encephalitis virus (strain Trinidad donkey)  
 OS Viruses; SRNA positive-strand viruses, no DNA stage; togaviridae;  
 OC Alphavirus.  
 OX NCBI\_TaxID=11038;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-86263392; PubMed=3098830;  
 RA Kinney R.M., Johnson B.J.B., Brown V.L., Trent D.W.;  
 RT "Nucleotide sequence of the 26 S mRNA of the virulent Trinidad donkey  
 strain of Venezuelan equine encephalitis virus and deduced sequence of  
 the encoded structural proteins.";  
 RT Vaccine derivative, strain TC-83.;  
 RT Virology 170:19-30(1989).  
 CC [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-89243175; PubMed=2124126;  
 RA Kinney R.M., Johnson B.J.B., Welch J.B., Tsuchiya K.R., Trent D.W.;  
 RT "The full-length nucleotide sequences of the virulent Trinidad donkey  
 strain of Venezuelan equine encephalitis virus and its attenuated  
 vaccine derivative, strain TC-83.";  
 RT Virology 170:19-30(1989).  
 CC -- FUNCTION: The capsid protein is an auto-protease.  
 CC -- PTM: Specific enzymatic cleavages in vivo yield mature proteins.  
 CC -- MISCELLANEOUS: The 6 kDa polypeptide probably serves as the signal  
 sequence for the membrane glycoprotein El, which is the viral  
 hemagglutinin.

-- SIMILARITY: The protease belongs to peptidase family S3.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 or send an email to license@isb-sib.ch).

CC

CC DR EMBL; M04937; AAA42997\_1; --  
 DR HSSP; P05674; IEP5.  
 DR MEROPS; S03\_001; --  
 DR InterPro; IPR002548; Alpha\_E1\_glycop.  
 DR InterPro; IPR000336; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR InterPro; IPR000336; Flavi\_glycoprot3.  
 DR InterPro; IPR000930; Peptidase\_S3.  
 DR InterPro; IPR000903; Pept\_Ser\_Cys.  
 DR Pfam; PF00944; Alpha\_core; 1.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
 DR PRINTS; PR00798; TOGAIRIN.  
 DR KW Coat protein; Glycoprotein; Hydrolase; Polyprotein; Serine protease;  
 KW Transmembrane.

FT CHAIN 1 275 Coat protein C.  
 FT CHAIN 276 334 Spike glycoprotein E3.  
 FT CHAIN 335 757 Spike glycoprotein E2.  
 FT CHAIN 758 812 6 kDa peptide.

FT ACT SITE 152 152 Charge relay system (By similarity).  
 FT ACT SITE 158 158 Charge relay system (By similarity).  
 FT ACT SITE 226 226 Charge relay system (By similarity).  
 FT TRANSMEM 702 718 Potential.

FT TRANSMEM 774 790



Query Match Best Local Similarity 57.9%; Pred. No. 1.5e+02; Matches 11; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

Qy 1 SSDGLWNNNQ---TQFL 15

Db 762 SLDBLWNNNQQMWTQI 780

RESULT 34

POLS\_EEVV3 STANDARD; PRT; 1255 AA.

ID P36329; DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-) (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2; 6 kDa peptide; Spike glycoprotein EI].

OS Venezuelan equine encephalitis virus (strain 3880).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus.

NCBI\_TaxID=36382; [1]

RN [1]

RX MEDLINE:93079859; PubMed=148915;

RA Kinney R.M., Tsuchiya K.R., Snelder J.M., Trent D.W.; RT "Genetic evidence that epizootic Venezuelan equine encephalitis (VEE) viruses may have evolved from enzootic VEE subtype I-D virus."; RL Virology 191:569-580(1992).

CC -!- FUNCTION: The capsid protein is an auto-protease.

CC -!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.  
CC -!- MISCELLANEOUS: The 6 kDa polypeptide probably serves as the signal sequence for the membrane glycoprotein EI, which is the viral hemagglutinin.

CC -!- SIMILARITY: The protease belongs to peptidase family S3.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; L00930; AACI9325.1; -. DR HSSP; P05674; IEP5. DR MEROPS; S03.001; -. DR InterPro; IPR002348; Alpha\_E1\_glycop. DR InterPro; IPR00936; Alpha\_E2\_glycop. DR InterPro; IPR00253; Alpha\_E3\_glycop. DR InterPro; IPR00336; Flavi\_glycoprote. DR InterPro; IPR00930; Peptidase\_S3. DR InterPro; IPR00903; Pept\_Ser\_Gly. DR Pfam; PF00944; Alpha\_core; 1. DR Pfam; PF01589; Alpha\_E1\_glycop; 1. DR Pfam; PF00943; Alpha\_E2\_glycop; 1. DR Pfam; PF01563; Alpha\_E3\_glycop; 1. DR PRINTS; PR00798; TOGA VIRIN. KW Coat protein; Glycoprotein; Hydrolase; Polyprotein; Serine protease; KW Transmembrane.

FT CHAIN 334 756 ENVELOPE GLYCOPROTEIN 2. FT CHAIN 757 812 6K POLYPEPTIDE N-terminus PRODUCT. FT CHAIN 813 1254 ENVLOPE GLYCOPROTEIN 1. SEQUENCE 138337 MW; 29DDEP375E92CAB CRC64;

Query Match Best Local Similarity 48.5%; Score 48; DB 2; Length 1254; Matches 11; Conservative 1; Mismatches 3; Indels 4; Gaps 1; Gaps 1;

Qy 1 SSDGLWNNNQ---TQFL 15

Db 762 SLDBLWNNNQQMWTQI 780

RESULT 35

POLS\_EEVVP STANDARD; PRT; 1255 AA.

ID P36332; DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-) (Capsid protein C); Spiky glycoprotein E3; Spike glycoprotein E2; 6 kDa peptide; Spike glycoprotein EI].

OS Venezuelan equine encephalitis virus (strain p676).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus.

NCBI\_TaxID=36385; [1]

RN [1]

RX MEDLINE:93079859; PubMed=148915;

RA Kinney R.M., Tsuchiya K.R., Snelder J.M., Trent D.W.; RT "Genetic evidence that epizootic Venezuelan equine encephalitis (VEE) viruses may have evolved from enzootic VEE subtype I-D virus."; RL Virology 191:569-580(1992).

CC -!- FUNCTION: The capsid protein is an auto-protease.

CC -!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.  
CC -!- MISCELLANEOUS: The 6 kDa polypeptide probably serves as the signal sequence for the membrane glycoprotein EI, which is the viral hemagglutinin.

CC -!- SIMILARITY: The protease belongs to peptidase family S3.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; L00930; AACI9319.1; -. DR HSSP; P05674; IEP5. DR MEROPS; S03.001; -. DR InterPro; IPR002348; Alpha\_E1\_glycop. DR InterPro; IPR00253; Alpha\_E2\_glycop. DR InterPro; IPR00336; Flavi\_glycoprote. DR InterPro; IPR00930; Peptidase\_S3. DR InterPro; IPR00903; Pept\_Ser\_Gly. DR Pfam; PF00944; Alpha\_core; 1. DR Pfam; PF01589; Alpha\_E1\_glycop; 1. DR Pfam; PF00943; Alpha\_E2\_glycop; 1. DR Pfam; PF01563; Alpha\_E3\_glycop; 1. DR PRINTS; PR00798; TOGA VIRIN. KW Coat protein; Glycoprotein; Hydrolase; Polyprotein; Serine protease; KW Transmembrane.

FT ACT\_SITE 158 158 Charge relay system (By similarity). FT ACT-SITE 226 226 Charge relay system (By similarity). FT TRANSMEM 702 722 Potential. FT TRANSMEM 795 814 Potential. FT TRANSMEM 1232 1249 N-Linked (GlcNAc. . .) (Potential). FT CARBOHYD 47 47 N-linked (GlcNAc. . .) (Potential). FT CARBOHYD 286 285 N-linked (GlcNAc. . .) (Potential). FT CARBOHYD 652 652 N-linked (GlcNAc. . .) (Potential). FT CARBOHYD 947 947 N-linked (GlcNAc. . .) (Potential). SEQUENCE 1255 AA; 138297 MW; 7D3J0E17CAEC310 CRC64;

Query Match Best Local Similarity 50.0%; Score 48; DB 1; Length 1255; Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SSDGLWNNNQ---TQFL 16

Db 763 SLDBLWNNNQQMWTQI 778



		Db	763	SLDHLMNNQQMFWIQ	778
DR	Pfam; PRO0943; Alpha_E2_glycop; 1.				
DR	Pfam; PRO1563; Alpha_E2_glycop; 1.				
DR	PRINTS; PR00798; TOGAVIRIN.				
KW	Polyprotein.				
SEQUENCE	1255 AA; 138564 MW; 9229511B3907A399 CRC64;				
QY	1 SSDGIWNNNQTOGLE 16				
Db	763 SLDHLMNNQQMFWIQ 778				
RESULT	38				
ID	036300	PRELIMINARY;	PRT;	1255 AA.	
AC	036300;				
DT	01-JAN-1998 (TREMBLrel. 05, Created)				
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Structural polyprotein.				
GN	Name=ns14;				
OS	Venezuelan equine encephalitis virus.				
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;				
OC	Alphavirus; VEEV complex.				
OX	NCBI_TaxID:11036;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Beck/Nycoff;				
RA	Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M., Smith J.F., Kang W., Sweeney W.P., Weaver S.C.;				
RT	"Repeated emergence of epidemic/epizootic Venezuelan equine encephalitis from a single genotype of enzootic subtype ID virus.";				
RT	J. Virol. 71:6697-6705(1997).				
RL	[2]				
RN	SEQUENCE FROM N.A.				
RP	STRAIN=Beck/Nycoff;				
RA	Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M., Smith J.F., Kang W., Sweeney W.P., Weaver S.C.;				
RA	Submitted (SERB-1998) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AR04471; AAC36374.1; -.				
DR	HSSP; P05674; IEPs.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:0019028; C:viral capsid; IEA.				
DR	GO; GO:0019031; C:viral envelope; IEA.				
DR	GO; GO:0004252; F:serine-type endopeptidase activity; IEA.				
DR	GO; GO:0005198; F:structural molecule activity; IEA.				
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR002248; Alpha_E1_glycop.				
DR	InterPro; IPR000336; Alpha_E2_glycop.				
DR	InterPro; IPR002333; Alpha_E3_glycop.				
DR	InterPro; IPR000336; Flavi_glycoprote.				
DR	InterPro; IPR000330; Peptidase_S3.				
DR	InterPro; IPR009033; Pept_Ser_Cys.				
DR	Pfam; PRO0944; Alpha_core; 1.				
DR	Pfam; PRO0944; Alpha_E1_glycop; 1.				
DR	Pfam; PRO0943; Alpha_E2_glycop; 1.				
DR	Pfam; PRO0943; Alpha_E3_glycop; 1.				
DR	PRINTS; PR00798; TOGAVIRIN.				
KW	Polyprotein.				
SEQUENCE	1255 AA; 138476 MW; 2CIECB6F196BC751 CRC64;				
QY	1 SSDGIWNNNQTOGLE 16				
Db	763 SLDHLMNNQQMFWIQ 778				
Query Match	48.5%; Score 48; DB 2; Length 1255;				
Best Local Similarity	50.0%; Pred. No. 1.5e+02;				
Matches	8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;				
QY	1 SSDGIWNNNQTOGLE 16				
FT	CHAIN 1 537 envelope glycoprotein E1.				
FT	CHAIN 1 537 envelope glycoprotein E2.				
SQ	SEQUENCE 1255 AA; 138458 MW; 8A73DC7501404C2 CRC64;				
Query Match	48.5%; Score 48; DB 2; Length 1255;				
Best Local Similarity	50.0%; Pred. No. 1.5e+02;				
Matches	8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;				

RESULT 40

091628 PRELIMINARY; PRT; 1255 AA.

ID 091628;

AC 091628;

DT 01-NOV-1998 (TREMBrel. 08, Created)

DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)

DE Structural polyprotein.

GN Name=n84;

OS Venezuelan equine encephalitis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage: Togaviridae;

OC Alphavirus; VEEV complex.

OX NCBI\_TaxID=11036;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=6921;

RX MEDLINE=9740681; PubMed=9261393;

RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M., Smith J.F., Kang W., Sweeney W.P., Weaver S.C.;

RT "Repeated emergence of epidemic/epizootic Venezuelan equine encephalitis from a single genotype of enzootic subtype ID virus.";

RL J. Virol. 71:6697-6705(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=6921;

RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M., Smith J.F., Kang W., Sweeney W.P., Weaver S.C.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AR004470; AAC36375.1; -

DR HSSP; P05674; IEP5;

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0004232; Fibrein-type endopeptidase activity; IEA.

DR GO; GO:0005198; Fibrillar structural molecule activity; IEA.

DR GO; GO:0005508; Peptidolysis; IEA.

DR InterPro; IPR002568; Alpha\_E1\_glycop.

DR InterPro; IPR000936; Alpha\_E2\_glycop.

DR InterPro; IPR002533; Alpha\_E3\_glycop.

DR InterPro; IPR003316; Flavi\_glycoprote.

DR InterPro; IPR000930; Peptidase\_S3.

DR InterPro; IPR00903; Pept\_Ser\_CYS.

DR Pfam; PRO0944; Alpha\_core; 1.

DR Pfam; PRO1589; Alpha\_E1\_glycop; 1.

DR Pfam; PRO0943; Alpha\_E2\_glycop; 1.

DR Pfam; PRO1563; Alpha\_E3\_glycop; 1.

DR PRIMIS; PR00198; TOGA VIRIN.

KW Polyprotein.

FT CHAIN 538 1255 envelope glycoprotein E1.

FT CHAIN 1 537 envelope glycoprotein E2.

SQ SEQUENCE 1255 AA; 138365 MW; F08FA923B9C0BA2 CRC64;

Query Match 48.5%; Score 48; DB 2; Length 1255;

Best local similarity 50.0%; Pred. No. 1.5e-02;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SSDGLWNNTQFLR 16

Db 763 SLDHHLWNNNQQMFWIQ 778

Search completed: December 30, 2004, 16:13:13  
Job time : 196 secs

*This Page Blank (uspto)*

Copyright (c) 1993 - 2004 Compugen Ltd.

Gencore version 5.1.6

Run on: December 30, 2004, 15:55:44 ; Search time 154 Seconds  
 (without alignments)  
 41.929 Million cell updates/sec

OM protein - protein search, using sw model

Title: US-10-718-321-1

Perfect score: 99

Sequence: 1 SSDGLIANNNQTLFLEHS 18

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 150 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseq1980s:\*

2: geneseq1990s:\*

3: geneseq2000s:\*

4: geneseq2001s:\*

5: geneseq2002s:\*

6: geneseq2003s:\*

7: geneseq2003s:\*

geneseq2004s:\*

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match Length	DB ID	Description
1	99	100.0	18	6 AA026687	Aaa26687 Human KIM
2	99	100.0	18	6 AA026673	Aao26673 Monoclonal
3	99	100.0	81	6 AA026678	Aao26678 Human KIM
4	99	100.0	263	7 ADE36629	Ade36629 Human NOV
5	99	100.0	263	7 ADE36622	Ade36622 Plasmid P
6	99	100.0	263	7 ADE36596	Ade36596 Human NOV
7	99	100.0	334	2 AAW3336	AAw3336 Human kid
8	99	100.0	334	6 AAO26679	Aao26679 KIM-1 rel
9	99	100.0	339	7 ADE36618	Ade36618 Plasmid P
10	99	100.0	339	7 ADE36592	Ade36592 Human NOV
11	99	100.0	339	6 ABB5592	Abb5592 Human can
12	99	100.0	359	6 ABP70439	Abp70439 Amino aci
13	99	100.0	359	6 ABP70438	Abp70438 Amino aci
14	99	100.0	359	6 ABR48174	Abr48174 Human bla
15	99	100.0	359	6 AAO26680	Aao26680 KIM-1 rel
16	99	100.0	359	7 ADE36594	Ade36594 Human NOV
17	99	100.0	359	7 ADN33522	Adn33522 Human can
18	99	100.0	364	6 ABP70443	Abp70443 Amino aci
19	99	100.0	364	6 ABP70442	Abp70442 Amino aci
20	99	100.0	365	6 ABP70440	Abp70440 Amino aci
21	94	94.9	359	6 ABP70441	Abp70441 Amino aci
22	84	84.8	451	2 AAR92803	Aar92803 Hepatitis
23	53	53.5	18	6 AAO26686	Aao26686 Human KIM
24	48	48.5	981	5 AAE13306	Aae13306 Venezuela
25	46	46.5	18	6 AAO26688	Aao26688 Human KIM

Result No.	Score	Query	Match Length	DB ID	Description
1	98	41.4	326	4 AAP60547	Aap60547 Segment 8
2	98	41.4	326	4 AAP60547	Aap60547 Segment 8
3	98	41.4	326	4 AAP60547	Aap60547 Segment 8
4	98	41.4	326	4 AAP60547	Aap60547 Segment 8
5	98	41.4	326	4 AAP60547	Aap60547 Segment 8
6	98	41.4	326	4 AAP60547	Aap60547 Segment 8
7	98	41.4	326	4 AAP60547	Aap60547 Segment 8
8	98	41.4	326	4 AAP60547	Aap60547 Segment 8
9	98	41.4	326	4 AAP60547	Aap60547 Segment 8
10	98	41.4	326	4 AAP60547	Aap60547 Segment 8
11	98	41.4	326	4 AAP60547	Aap60547 Segment 8
12	98	41.4	326	4 AAP60547	Aap60547 Segment 8
13	98	41.4	326	4 AAP60547	Aap60547 Segment 8
14	98	41.4	326	4 AAP60547	Aap60547 Segment 8
15	98	41.4	326	4 AAP60547	Aap60547 Segment 8
16	98	41.4	326	4 AAP60547	Aap60547 Segment 8
17	98	41.4	326	4 AAP60547	Aap60547 Segment 8
18	98	41.4	326	4 AAP60547	Aap60547 Segment 8
19	98	41.4	326	4 AAP60547	Aap60547 Segment 8
20	98	41.4	326	4 AAP60547	Aap60547 Segment 8
21	98	41.4	326	4 AAP60547	Aap60547 Segment 8
22	98	41.4	326	4 AAP60547	Aap60547 Segment 8
23	98	41.4	326	4 AAP60547	Aap60547 Segment 8
24	98	41.4	326	4 AAP60547	Aap60547 Segment 8
25	98	41.4	326	4 AAP60547	Aap60547 Segment 8

Result No.	Score	Query	Match Length	DB ID	Description
1	98	41.4	326	4 AAP60547	Aap60547 Segment 8
2	98	41.4	326	4 AAP60547	Aap60547 Segment 8
3	98	41.4	326	4 AAP60547	Aap60547 Segment 8
4	98	41.4	326	4 AAP60547	Aap60547 Segment 8
5	98	41.4	326	4 AAP60547	Aap60547 Segment 8
6	98	41.4	326	4 AAP60547	Aap60547 Segment 8
7	98	41.4	326	4 AAP60547	Aap60547 Segment 8
8	98	41.4	326	4 AAP60547	Aap60547 Segment 8
9	98	41.4	326	4 AAP60547	Aap60547 Segment 8
10	98	41.4	326	4 AAP60547	Aap60547 Segment 8
11	98	41.4	326	4 AAP60547	Aap60547 Segment 8
12	98	41.4	326	4 AAP60547	Aap60547 Segment 8
13	98	41.4	326	4 AAP60547	Aap60547 Segment 8
14	98	41.4	326	4 AAP60547	Aap60547 Segment 8
15	98	41.4	326	4 AAP60547	Aap60547 Segment 8
16	98	41.4	326	4 AAP60547	Aap60547 Segment 8
17	98	41.4	326	4 AAP60547	Aap60547 Segment 8
18	98	41.4	326	4 AAP60547	Aap60547 Segment 8
19	98	41.4	326	4 AAP60547	Aap60547 Segment 8
20	98	41.4	326	4 AAP60547	Aap60547 Segment 8
21	98	41.4	326	4 AAP60547	Aap60547 Segment 8
22	98	41.4	326	4 AAP60547	Aap60547 Segment 8
23	98	41.4	326	4 AAP60547	Aap60547 Segment 8
24	98	41.4	326	4 AAP60547	Aap60547 Segment 8
25	98	41.4	326	4 AAP60547	Aap60547 Segment 8

Result No.	Score	Query	Match Length	DB ID	Description
1	98	41.4	326	4 AAP60547	Aap60547 Segment 8
2	98	41.4	326	4 AAP60547	Aap60547 Segment 8
3	98	41.4	326	4 AAP60547	Aap60547 Segment 8
4	98	41.4	326	4 AAP60547	Aap60547 Segment 8
5	98	41.4	326	4 AAP60547	Aap60547 Segment 8
6	98	41.4	326	4 AAP60547	Aap60547 Segment 8
7	98	41.4	326	4 AAP60547	Aap60547 Segment 8
8	98	41.4	326	4 AAP60547	Aap60547 Segment 8
9	98	41.4	326	4 AAP60547	Aap60547 Segment 8
10	98	41.4	326	4 AAP60547	Aap60547 Segment 8
11	98	41.4	326	4 AAP60547	Aap60547 Segment 8
12	98	41.4	326	4 AAP60547	Aap60547 Segment 8
13	98	41.4	326	4 AAP60547	Aap60547 Segment 8
14	98	41.4	326	4 AAP60547	Aap60547 Segment 8
15	98	41.4	326	4 AAP60547	Aap60547 Segment 8
16	98	41.4	326	4 AAP60547	Aap60547 Segment 8
17	98	41.4	326	4 AAP60547	Aap60547 Segment 8
18	98	41.4	326	4 AAP60547	Aap60547 Segment 8
19	98	41.4	326	4 AAP60547	Aap60547 Segment 8
20	98	41.4	326	4 AAP60547	Aap60547 Segment 8
21	98	41.4	326	4 AAP60547	Aap60547 Segment 8
22	98	41.4	326	4 AAP60547	Aap60547 Segment 8
23	98	41.4	326	4 AAP60547	Aap60547 Segment 8
24	98	41.4	326	4 AAP60547	Aap60547 Segment 8
25	98	41.4	326	4 AAP60547	Aap60547 Segment 8

99	41	41-4	326	7	ADB336761	PN
100	41	41-4	399	4	ABG19483	XX
101	41	41-4	487	4	AAM0109	PD
102	41	41-4	494	5	ABE53478	XX
103	41	41-4	540	8	ADU48637	PF
104	41	41-4	542	8	ADU48615	XX
105	41	41-4	569	6	ABU35742	PR
106	41	41-4	602	4	ABG07448	PR
107	41	41-4	624	5	ABT7354	XX
108	41	41-4	721	7	ADU70091	PA
109	41	41-4	790	4	ADU3243	PA
110	41	41-4	790	5	ABE23390	XX
111	41	41-4	790	7	ADB75262	PI
112	41	41-4	871	3	ABP41558	XX
113	41	41-4	871	4	ABM38935	DR
114	41	41-4	925	2	ABR21605	XX
115	41	41-4	927	6	ABU11694	PT
116	41	41-4	947	3	ABU11527	PT
117	41	41-4	956	3	ABY94752	PT
118	41	41-4	1281	5	ABQ32157	PT
119	41	41-4	1350	4	AAU02944	XX
120	41	41-4	1455	2	ABR23824	PS
121	41	41-4	1464	2	ABR5529	XX
122	41	41-4	1464	2	ABR80970	CC
123	41	41-4	1464	2	ABR8576	CC
124	41	41-4	1464	2	ABW85576	CC
125	41	41-4	1464	3	AAV56113	CC
126	41	41-4	1464	3	ABR26215	CC
127	41	41-4	1464	5	ABR56507	CC
128	41	41-4	1464	5	AAQ18063	CC
129	41	41-4	1464	5	ABG32158	CC
130	41	41-4	1464	6	ABU65878	XX
131	41	41-4	1464	6	ABU61423	SQ
132	41	41-4	1464	6	ABU03578	Sequence 18 AA:
133	41	41-4	1464	6	ABU03574	Query Match
134	41	41-4	1464	6	ABU03577	Best Local Similarity
135	41	41-4	1464	6	ABU03572	100.0%; Score 99;
136	41	41-4	1464	6	ABU03579	DB 6; Length 18;
137	41	41-4	1464	6	ABU03571	Mismatches 0;
138	41	41-4	1464	6	ABU03576	Indels 0;
139	41	41-4	1464	6	ABU03580	Gaps 0;
140	41	41-4	1464	6	ABU03570	
141	41	41-4	1464	6	ABU03577	RESULT 2
142	41	41-4	1464	6	ABU03560	AA026673
143	41	41-4	1464	6	ABO43070	ID AD026673 standard; peptide: 18 AA.
144	41	41-4	1464	7	ABE39234	XX
145	41	41-4	1970	4	ABE64827	AC
146	40	40-4	126	8	ADL05841	AA026673;
147	40	40-4	141	3	AAQ01614	XX
148	40	40-4	149	4	ABG05062	DT 20-MAR-2003 (first entry)
149	40	40-4	161	2	ABR93597	XX
150	40	40-4	161	2	ABR93595	DB Monoclonal antibody binding epitope, SEQ ID No 1.
						XX
						Cytostatic; gene therapy; antibody; antigen; antigen-binding; proteolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer; binding epitope.
						XX
						KW
						Renal disease; injury; renal cancer; binding epitope.
						XX
						OS Homo sapiens.
						XX
						PN WO200298920-A1.
						XX PD 12-DEC-2002.
						XX PF 31-MAY-2002; 2002WO-US017402.
						XX PR 01-JUN-2001; 2001US-0295449P.
						XX PR 04-JUN-2001; 2001US-0295907P.
						XX (BIOJ ) BIOMAN INC.
						XX PA (GEHO ) GEN HOSPITAL CORP.
						XX PI Bailly V, Bonventre J;
						XX IS Synthetic.

DR WPI; 2003-156845/15.  
 XX  
 PT New antibody, antibody derivative or antigen-binding polypeptide that  
 PT inhibits proteolytic release of a soluble kidney injury molecule-1  
 PT polypeptide, useful for treating or preventing renal disease or injury,  
 PT e.g. renal cancer.  
 XX  
 PS Claim 4; Page 25; 42pp; English.

CC The invention relates to a novel antibody, antibody derivative or antigen  
 CC -binding polypeptide that inhibits proteolytic release of a soluble  
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.  
 CC The antibody, antibody derivative or antigen-binding polypeptide is  
 CC useful for treating or preventing renal disease or injury, e.g. renal  
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1  
 CC polypeptide. This sequence represents a binding epitope of the invention  
 XX  
 SQ Sequence 18 AA:

Query Match	100.0%	Score	99;	DB	6;	Length	81;	
Best Local Similarity	100.0%	Pred.	No.	2.3e-07;	Indels	0;	Gaps	0;
Matches	18;	Conservative	0;	Mismatches	0;			
Qy	1 SSDGLWNNNQTLFLEHS 18							
Db	55 SSDGLWNNNQTLFLEHS 72							

RESULT 3  
 ID A026678 standard; protein; 81 AA.  
 XX  
 AC A026678;  
 XX  
 DT 20-MAR-2003 (first entry)  
 XX  
 DE Human KIM-1 mucin domain protein, SEQ ID No 6.  
 XX  
 KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;  
 KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;  
 KW renal disease; injury; renal cancer; human.  
 OS Homo sapiens.  
 XX  
 PN WO20020298920-A1.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 31-MAY-2002; 2002WO-US017402.  
 XX  
 PR 01-JUN-2001; 2001US-0295449P.  
 XX  
 PA (BIO) BIOPHARM INC.  
 PA (BIO ) GRN HOSPITAL CORP.  
 XX  
 PT Bailly V, Bonventre J;  
 XX  
 DR WPI; 2003-156845/15.  
 XX  
 PT New antibody, antibody derivative or antigen-binding polypeptide that  
 PT inhibits proteolytic release of a soluble kidney injury molecule-1  
 PT polypeptide, useful for treating or preventing renal disease or injury,  
 PT e.g. renal cancer.  
 XX  
 PS Disclosure; Fig 1A; 42pp; English.

CC The invention relates to a novel antibody, antibody derivative or antigen  
 CC -binding polypeptide that inhibits proteolytic release of a soluble  
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.  
 CC The antibody, antibody derivative or antigen-binding polypeptide is  
 CC useful for treating or preventing renal disease or injury, e.g. renal  
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1  
 CC polypeptide. This sequence represents a human KIM-1 mucin domain protein  
 CC of the invention

CC polypeptide. This sequence represents a human KIM-1 mucin domain protein  
 CC of the invention  
 XX  
 SQ Sequence "81 AA;"

Query Match	100.0%	Score	99;	DB	6;	Length	81;	
Best Local Similarity	100.0%	Pred.	No.	2.3e-07;	Indels	0;	Gaps	0;
Matches	18;	Conservative	0;	Mismatches	0;			
Qy	1 SSDGLWNNNQTLFLEHS 18							
Db	55 SSDGLWNNNQTLFLEHS 72							

RESULT 4  
 ID ADE36629 standard; protein; 263 AA.  
 XX  
 AC ADE36629;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOV1C protein SEQ ID NO:39.  
 XX  
 KW human; NOV1; cytostatic; antiinflammatory; gene therapy; vaccine;  
 KW renal cancer; inflammation; tissue typing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200300856-A2.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PR 19-MAR-2003; 2003WO-US008490.  
 XX  
 PR 19-MAR-2002; 2002US-0365491P.  
 XX  
 PR 13-SEP-2002; 2002US-0410618P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PT Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Mesri M,  
 PT Ooi CB, Anderson DW, Guo X, Giot L, Starling G;  
 XX  
 DR WPI; 2003-876927/81.  
 XX  
 PT New polypeptide, useful for preparing a composition for treating or  
 PT preventing a pathology associated with NOV1 polypeptide e.g. renal cancer  
 PT or inflammation, or for tissue typing.  
 XX  
 PS Example 9; SBQ ID NO 39; 239pp; English.

CC The present invention describes an isolated human NOV1 polypeptide, where  
 CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at  
 CC least 95 % identical to it, or a sequence comprising one or more  
 CC conservative substitutions in the amino acid sequence. The NOV1  
 CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and  
 CC antiinflammatory activities, and can be used in gene therapy, and in  
 CC vaccines. The NOV1 polypeptide is useful for preparing a composition for  
 CC treating or preventing a pathology associated with NOV1 polypeptide e.g.  
 CC renal cancer or inflammation, or for tissue typing. The present sequence  
 CC represents a protein sequence which is used in an example from the  
 CC present invention.

XX  
 SQ Sequence 263 AA;

Query Match	100.0%	Score	99;	DB	7;	Length	263;	
Best Local Similarity	100.0%	Pred.	No.	8.2e-07;	Indels	0;	Gaps	0;
Matches	18;	Conservative	0;	Mismatches	0;			
Qy	1 SSDGLWNNNQTLFLEHS 18							
Db	244 SSDGLWNNNQTLFLEHS 261							

**RESULT 5**  
 XX ADE3622  
 ID ADE3622 standard; protein; 263 AA.  
 XX  
 AC ADE36622;  
 XX DT 29-JAN-2004 (first entry)  
 XX PD 02-OCT-2003.  
 XX PR 19-MAR-2003; 2003WO-US008490.  
 XX PT 19-MAR-2002; 2002US-0365491P.  
 XX PR 13-SEP-2002; 2002US-0410618P.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Meari M; Ooi CB, Anderson DW, Guo X, Giot L, Starling G;  
 XX DR WPI; 2003-876927/81.  
 XX N-PSDB; ADE36621.  
 XX PT New polypeptide, useful for preparing a composition for treating or preventing a pathology associated with NOVX polypeptide e.g. renal cancer or inflammation, or for tissue typing.  
 XX PT New polypeptide, useful for preparing a composition for treating or preventing a pathology associated with NOVX polypeptide e.g. renal cancer, or inflammation, or for tissue typing.  
 XX PS Example 2; SEQ ID NO 32; 239pp; English.

CC The present invention describes an isolated human NOVX polypeptide, where CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at least 95 % identical to it, or a sequence comprising one or more conservative substitutions in the amino acid sequence encoding it. The NOVX CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and antiinflammatory activities, and can be used in gene therapy, and in vaccines. The NOVX polypeptide is useful for preparing a composition for CC treating or preventing a pathology associated with NOVX polypeptide e.g. renal cancer or inflammation, or for tissue typing. The present sequence CC represents human NOVIC from the present invention.  
 XX Sequence 263 AA;

Query Match 100.0%; Score 99; DB 7; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSDGILWNNTQQLFLEHS 18  
 Db 244 SSDGILWNNTQQLFLEHS 261

**RESULT 6**  
 XX ADE36596  
 ID ADE36596 standard; protein; 263 AA.  
 XX AC ADE36596;  
 XX DT 29-JAN-2004 (first entry)  
 XX PR Human Novic protein SEQ ID NO:6.  
 XX OS Homo sapiens.

XX WO2003080856-A2.  
 XX PD 02-OCT-2003.  
 XX PR 19-MAR-2003; 2003WO-US008490.  
 XX PT 19-MAR-2002; 2002US-0365491P.  
 XX PR 13-SEP-2002; 2002US-0410618P.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Meari M; Ooi CB, Anderson DW, Guo X, Giot L, Starling G;  
 XX DR WPI; 2003-876927/81.  
 XX N-PSDB; ADE36595.

CC The present invention describes an isolated human NOVX polypeptide, where CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at least 95 % identical to it, or a sequence comprising one or more conservative substitutions in the amino acid sequence encoding it. The NOVX CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and antiinflammatory activities, and can be used in gene therapy, and in vaccines. The NOVX polypeptide is useful for preparing a composition for CC treating or preventing a pathology associated with NOVX polypeptide e.g. renal cancer or inflammation, or for tissue typing. The present sequence CC represents human NOVIC from the present invention.  
 XX Sequence 263 AA;

Query Match 100.0%; Score 99; DB 7; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSDGILWNNTQQLFLEHS 18  
 Db 244 SSDGILWNNTQQLFLEHS 261

**RESULT 7**  
 XX AAWJ8336  
 ID AAWJ8336 standard; protein; 334 AA.  
 XX AC AAWJ8336;  
 XX DT 21-MAY-1998 (first entry)  
 XX DE Human kidney injury related molecule (KIM).  
 XX  
 XX Kidney injury related molecule; KIM; human; renal disease; injury; nephritis; tissue regeneration; therapy; monoclonal antibody.  
 XX OS Homo sapiens.  
 XX PN WO9744460-A1.  
 XX PD 27-NOV-1997.  
 XX PR 23-MAY-1997; 97WO-US009303.  
 XX PR 24-MAY-1996; 96US-0018228P.  
 XX PR 23-AUG-1996; 96US-0023442P.

PR 04-JUN-2001; 2001US-0295907P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Sanicola-Nadel, M, Bonventre JV, Hession CA, Ichimura T, Wei H;  
 PI Cate RL;  
 XX DR WPI; 1998-018514/02.  
 XX  
 PT DNA encoding kidney injury related molecule - which is upregulated in injured or regenerating tissue, useful to promote growth of new tissue and survival of damaged tissue.  
 XX  
 PS Claim 9; Page 46-47; 69pp; English.  
 XX  
 CC This protein, designated kidney injury related molecule (KIM), is up-regulated in injured or regenerating tissue. Its amino acid sequence was deduced from a clone (see ATG6055) obtained from a human embryonic liver library. A 572-amino acid (see AW3834) and a 307-amino acid rat KIM (see AW3834) are also claimed. Recombinant KIM polypeptides can be expressed in prokaryotic and eukaryotic host cells using a claimed process. Soluble variants fused to a toxin, imageable compound or radionuclide, and IgG fusion proteins are also claimed. KIM, or an agonist, can be used to treat renal disease and to promote the growth of new tissue or the survival of damaged tissue, generally in conditions where the binding of specific ligand to KIM stimulates cell growth, maintains cellular differentiation or reduces apoptosis, e.g. in cases of renal failure, nephritis, kidney transplants, toxic or hypoxic injury. A monoclonal antibody specific for KIM can be used to treat renal disease, e.g. where binding of KIM to ligand results in neoplasia, loss of cellular function, susceptibility to apoptosis or promotion of inflammation, deliver imaging agents to KIM expressing cells in vivo or in vitro and measure KIM concentration by immunoassay.  
 CC Damage/Regeneration of renal cells can be determined by measuring KIM, particularly to diagnose or monitor the progress of disease or therapy. KIM-expressing tumour cells can be inhibited by treatment with a fusion protein comprising KIM ligand or Mab with a toxin or radionuclide, and tumour cells that express KIM ligand can be inhibited with similarly tagged KIM or anti-KIM ligand antibody  
 XX SQ Sequence 334 AA:  
 Query Match 100.0%; Score 99; DB 2; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGILWNNNQTQLEHS 18  
 DB 264 SSDGILWNNNQTQLEHS 281  
 RESULT 9  
 ID ADB36618  
 ID ADB36618 standard; protein; 339 AA.  
 AC ADB36618;  
 AC DT 29-JAN-2004 (first entry)  
 XX DE Plasmid pCR2.1-CG57008-03-S843 15B protein insert SEQ ID NO:28.  
 XX human; NOX; cytotoxic; antiinflammatory; gene therapy; vaccine;  
 KW renal; cancer; inflammation; tissue typing.  
 XX Synthetic.  
 OS Homo sapiens.  
 PN WO2003080856-A2.  
 XX PD 02-OCT-2003.  
 XX PP 19-MAR-2003; 2003WO-US008490.  
 XX PR 19-MAR-2002; 2002US-0365491P.  
 PR 13-SEP-2002; 2002US-0410618P.  
 XX (CURA-) CURAGEN CORP.  
 XX Legley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Mesri M;  
 PR Ooi CB, Anderson DW, Guo X, Giot L, Starling G;  
 XX WPI; 2003-876927/81.  
 DR N-PSDB; ADB36617.  
 XX  
 PT New polypeptide, useful for preparing a composition for treating or preventing a pathology associated with NOX polypeptide e.g. renal cancer or inflammation, or for tissue typing.  
 XX PR 31-MAY-2002; 2002WO-US017402.  
 XX PR 01-JUN-2001; 2001US-0295449P.

PS Example 1; SEQ ID NO 28; 239pp; English.

XX

CC The present invention describes an isolated human NOVX polypeptide, where

CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at

CC least 95 % identical to it, or a sequence comprising one or more

CC conservative substitutions in the amino acid sequence. The NOVX

CC polypeptide, and nucleic acid sequence encoding it, has cytosstatic and

CC antiinflammatory activities, and can be used in gene therapy, and in

CC vaccines. The NOVX polypeptide is useful for preparing a composition for

CC treating or preventing a pathology associated with NOVX polypeptide e.g.

CC renal cancer or inflammation, or for tissue typing. The present sequence

CC represents a PCR2.1-CG57008-03-SB43 15B protein insert, which is used in

CC an example from the present invention.

XX

SQ Sequence 339 AA;

Query Match 100.0%; Score 99; DB 7; Length 339;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSDGIWNNNOTQLEHs 18

Db 244 SSDGIWNNNOTQLEHs 261

RESULT 10

ID ADE36592

ID ADE36592 standard; protein; 339 AA.

XX

AC ADE36592;

XX

DT 29-JAN-2004 (First entry)

XX

DE Human NOVIA protein SEQ ID NO:2.

XX

KW human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;

KW renal cancer; inflammation; tissue typing.

XX

OS Homo sapiens.

XX

PN WO2003025138-A2.

XX

PD 27-MAR-2003.

XX

PR 17-SEP-2002; 2002WO-US029560.

XX

PR 17-SEP-2001; 2001US-0323463P.

PR 20-SEP-2001; 2001US-0323887P.

PR 13-NOV-2001; 2001US-0350665P.

PR 08-FEB-2002; 2002US-0355145P.

PR 08-FEB-2002; 2002US-0355257P.

PR 12-APR-2002; 2002US-0372246P.

XX

PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX

PI Afar D, Aziz N, Gish KC, Hevezsi PA, Mack DH, Wilson KE;

XX

PI Zlotnick A;

XX

DR WPI; 2003-354600/33.

XX

N-PSDB; ACCT2709.

XX

PT New genes that are up-regulated or down-regulated in cancers, useful as

PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as

PT therapeutic targets for screening drugs for treating these diseases.

XX

PS Claim 12; Page 742; 767pp; English.

XX

The present invention describes an isolated nucleic acid molecule, which

CC comprises the sequence of any of the genes that are up-regulated or down-

CC regulated in specific cancers (e.g. about 1031 genes up-regulated in

CC acute lymphocytic Leukemia). ACC72641 to ACC72660 represent cancer

CC related gene nucleotide sequences which encode the proteins given in

CC ABR58521 to ABR58709. Also described: (1) determining the presence or

CC absence of a pathological cell in a patient; (2) an expression vector

CC comprising a nucleic acid molecule described above; (3) a host cell

CC comprising the vector; (4) an isolated polypeptide, which is encoded by

CC the nucleic acid; (5) an antibody that specifically binds the polypeptide

CC of (4); (6) specifically targeting a compound to a pathological cell in a

CC patient by administering to the patient the antibody above; and (7) a

CC drug screening assay. The nucleic acid is useful as diagnostic markers or

CC therapeutic targets. In particular, the nucleic acid is useful for

CC diagnosing a pathology, e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,

CC pancreas, prostate, skin and uterus; wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in

CC drug screening, particularly for identifying agents for treating these

CC represents human NOVIA from the present invention.

CC pathologies  
 XX SQ Sequence 359 AA;

Query Match 100.0%; Score 99; DB 6; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 SSDGLWNNNOTQFLLEHS 18  
 Db 264 SSDGLWNNNOTQFLLEHS 281

RESULT 12  
 ABP70439 ID ABP70439 standard; protein; 359 AA.  
 XX AC ABP70439;  
 XX DT 22-APR-2003 (first entry)  
 XX DE Amino acid sequence of human TIM-1 allele 1.  
 XX KW T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;  
 KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;  
 KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;  
 KW allergic T cell response; autoimmune disease.  
 XX OS Homo sapiens.  
 XX PN WO200302722-A2.  
 XX PD 09-JAN-2003.  
 XX PP 01-JUL-2002; 2002WO-US020890.  
 XX PR 29-JUN-2001; 2001US-0302344P.  
 XX PA (STRD ) UNIV LEELAND STANFORD JUNIOR.  
 XX PI McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;  
 XX DR WPI: 2003-210268/20.  
 XX DR N-PSDB; ABZ68332.  
 XX PT New nucleic acid comprising a mammalian T cell Immunoglobulin domain and  
 PT Mucin domain gene sequences, useful for treating cancer or asthma,  
 PT allergy, eczema or autoimmune disease.  
 XX PS Claim 10; Page 80-81; 94pp; English.  
 XX CC The present sequence is a human T cell immunoglobulin domain and mucin  
 CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,  
 CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with  
 CC conserved IgV and mucin domains. The locus comprising the TIM family is  
 CC genetically associated with immune dysfunction, including asthma. The TIM  
 CC gene family is located within a region of human chromosome 5 that is  
 CC commonly deleted in malignancies and myelodysplastic syndrome. Variants  
 CC of TIM-1 and TIM-3 are associated with susceptibility to airway  
 CC hyperreactivity and allergic T cell responses, and other variants  
 CC associated with protection against these responses. T cells express TIM  
 CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells  
 CC preferentially express TIM-3, while Th2 cells preferentially express TIM-  
 CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,  
 CC asthma, allergies, eczema or autoimmune diseases  
 XX SQ Sequence 359 AA;

Query Match 100.0%; Score 99; DB 6; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 SSDGLWNNNOTQFLLEHS 18  
 Db 264 SSDGLWNNNOTQFLLEHS 281

RESULT 13  
 ABP70438 ID ABP70438 standard; protein; 359 AA.  
 XX AC ABP70438;  
 XX DT 22-APR-2003 (first entry)  
 XX DE Amino acid sequence of human TIM-1 allele 1.  
 XX KW T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;  
 KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;  
 KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;  
 KW allergic T cell response; autoimmune disease.  
 XX OS Homo sapiens.  
 XX PN WO200302722-A2.  
 XX PD 09-JAN-2003.  
 XX PP 01-JUL-2002; 2002WO-US020890.  
 XX PR 29-JUN-2001; 2001US-0302344P.  
 XX PA (STRD ) UNIV LEELAND STANFORD JUNIOR.  
 XX PI McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;  
 XX DR N-PSDB; ABZ68332.

Query Match 100.0%; Score 99; DB 6; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 SSDGLWNNNOTQFLLEHS 18  
 Db 264 SSDGLWNNNOTQFLLEHS 281

XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Human bladder cancer associated protein sequence SEQ ID NO:64.  
 XX  
 KW Human; bladder cancer; cytostatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003003906-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PR 03-JUL-2002; 2002WO-US021338.  
 XX  
 PR 03-JUL-2001; 2001US-0302814P.  
 XX  
 PR 03-AUG-2001; 2001US-0310099P.  
 XX  
 PR 08-NOV-2001; 2001US-0341705P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 PI Mack DH, Aziz N;  
 XX  
 DR WPI; 2003-201532/19.  
 DR N-PADB; ACC50985.  
 XX  
 PT Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.  
 XX  
 PS Claim 10; Page 252; 307pp; English.  
 CC The present invention describes a method for detecting a bladder cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a table of Sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancer-associated proteins given in ADR48146 to ABP48242. Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications  
 CC Sequence 359 AA;  
 SQ

Query Match	100.0%	Score	99	DB	6	Length	359
Best Local Similarity	100.0%	Pred.	No.	1.1e-05			
Matches	18	Conservative	0	Mismatches	0	Indels	0
Gaps	0						

Qy 1 SSDGLWNNTQLEHS 18  
 Db 264 SSDGLWNNTQLEHS 281

RESULT 15  
 ADR36594  
 ID ADR36594 standard; protein; 359 AA.  
 XX  
 AC ADR36594;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOV1b protein SEQ ID NO:4.  
 XX  
 KW human; NOV1b; cytostatic; antiinflammatory; gene therapy; vaccine; renal; cancer; inflammation; tissue typing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20030080856-A2.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PR 19-MAR-2003; 2003WO-US008490.  
 XX  
 PR 19-MAR-2002; 2002US-0365491P.  
 XX  
 PR 13-SEP-2002; 2002US-0410618P.  
 XX  
 PA (CURA-) CURAGEN CORP.

KW renal disease; injury; renal cancer; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200298920-A1.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PR 31-MAY-2002; 2002WO-US017402.  
 XX  
 PR 01-JUN-2001; 2001US-0295449P.  
 PR 04-JUN-2001; 2001US-0285907P.  
 XX  
 (BIOT ) BIOPHAR INC.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PT Bailly V, Bonventre J;  
 XX  
 DR WPI; 2003-156845/15.  
 XX  
 PT New antibody, antibody derivative or antigen-binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 polypeptide, useful for treating or preventing renal disease or injury, e.g. renal cancer.  
 XX  
 PT Disclosure; Page 40-41; 42pp; English.  
 XX  
 CC The invention relates to a novel antibody derivative or antigen -binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.  
 CC The antibody, antibody derivative or antigen-binding polypeptide is useful for treating or preventing renal disease or injury, e.g. renal cancer. The antibody is also useful for inhibiting shedding of the KIM-1 polypeptide. This sequence represents a protein relating to the KIM-1 protein of the invention  
 XX  
 Sequence 359 AA;

Query Match	100.0%	Score	99	DB	6	Length	359
Best Local Similarity	100.0%	Pred.	No.	1.1e-05			
Matches	18	Conservative	0	Mismatches	0	Indels	0
Gaps	0						

Qy 1 SSDGLWNNTQLEHS 18  
 Db 264 SSDGLWNNTQLEHS 281

RESULT 16  
 ADR36594  
 ID ADR36594 standard; protein; 359 AA.  
 XX  
 AC ADR36594;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOV1b protein SEQ ID NO:4.  
 XX  
 KW human; NOV1b; cytostatic; antiinflammatory; gene therapy; vaccine; renal; cancer; inflammation; tissue typing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20030080856-A2.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PR 19-MAR-2003; 2003WO-US008490.  
 XX  
 PR 19-MAR-2002; 2002US-0365491P.  
 XX  
 PR 13-SEP-2002; 2002US-0410618P.  
 XX  
 PA (CURA-) CURAGEN CORP.

RESULT 15  
 ADR36594  
 ID ADR36594 standard; protein; 359 AA.  
 XX  
 AC ADR36594;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOV1b protein SEQ ID NO:4.  
 XX  
 KW human; NOV1b; cytostatic; antiinflammatory; gene therapy; vaccine; renal; cancer; inflammation; tissue typing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20030080856-A2.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PR 19-MAR-2003; 2003WO-US008490.  
 XX  
 PR 19-MAR-2002; 2002US-0365491P.  
 XX  
 PR 13-SEP-2002; 2002US-0410618P.  
 XX  
 PA (CURA-) CURAGEN CORP.

Qy 1 SSDGLWNNTQLEHS 18  
 Db 264 SSDGLWNNTQLEHS 281

RESULT 15  
 ADR36594  
 ID ADR36594 standard; protein; 359 AA.  
 XX  
 AC ADR36594;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOV1b protein SEQ ID NO:4.  
 XX  
 KW human; NOV1b; cytostatic; antiinflammatory; gene therapy; vaccine; renal; cancer; inflammation; tissue typing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20030080856-A2.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PR 19-MAR-2003; 2003WO-US008490.  
 XX  
 PR 19-MAR-2002; 2002US-0365491P.  
 XX  
 PR 13-SEP-2002; 2002US-0410618P.  
 XX  
 PA (CURA-) CURAGEN CORP.

Qy 1 SSDGLWNNTQLEHS 18  
 Db 264 SSDGLWNNTQLEHS 281

PI Lepley DM, Rieger DK, Tse K, Restelli L, Smithson G, Mesri M; PR 05-JUN-2002; 2002US-0386614P.  
 PI Ooi CE, Anderson DW, Guo X, Giot L, Starling G; PR 16-JUL-2002; 2002US-0396839P.  
 XX WPI: 2003-876227/81. PR 22-JUL-2002; 2002US-0397775P.  
 DR N-PSDB; ADB36593. PR 22-JUL-2002; 2002US-0397845P.  
 XX PT New polypeptide, useful for preparing a composition for treating or PR 09-SBP-2002; 2002US-0409450P.  
 PT preventing a pathology associated with NOVX polypeptide e.g. renal cancer. PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 PT or inflammation, or for tissue typing. XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezzi PA;  
 XX PS Claim 1; SEQ ID NO 4; 239pp; English. PR Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
 XX CC The present invention describes an isolated human NOVX polypeptide, where PR DR N-PSDB; ADN38983.  
 CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at PR XX Best local Similarity 100.0%; Pred. No. 1.1e-06;  
 CC conservative substitutions in the amino acid sequence. The NOVX PR Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and PR QY 1 SSDGLWNNTQOLFLEHS 18  
 CC antiinflammatory activities, and can be used in gene therapy, and in PR Db 264 SSDGLWNNTQOLFLEHS 281  
 Sequence 359 AA;

RESULT 17

Query Match 100.0%; Score 99; DB 7; Length 359; PR XX  
 Best local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQOLFLEHS 18  
 Db 264 SSDGLWNNTQOLFLEHS 281

RESULT 18

Query Match 100.0%; Score 99; DB 7; Length 359; PR XX  
 Best local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQOLFLEHS 18  
 Db 264 SSDGLWNNTQOLFLEHS 281  
 Sequence 359 AA;

RESULT 19

Query Match 100.0%; Score 99; DB 7; Length 359; PR XX  
 Best local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQOLFLEHS 18  
 Db 264 SSDGLWNNTQOLFLEHS 281  
 Sequence 359 AA;

RESULT 20

Query Match 100.0%; Score 99; DB 7; Length 359; PR XX  
 Best local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQOLFLEHS 18  
 Db 264 SSDGLWNNTQOLFLEHS 281  
 Sequence 359 AA;

RESULT 21

Query Match 100.0%; Score 99; DB 7; Length 359; PR XX  
 Best local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQOLFLEHS 18  
 Db 264 SSDGLWNNTQOLFLEHS 281  
 Sequence 359 AA;

RESULT 22

Query Match 100.0%; Score 99; DB 7; Length 359; PR XX  
 Best local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQOLFLEHS 18  
 Db 264 SSDGLWNNTQOLFLEHS 281  
 Sequence 359 AA;

RESULT 23

Query Match 100.0%; Score 99; DB 7; Length 359; PR XX  
 Best local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQOLFLEHS 18  
 Db 264 SSDGLWNNTQOLFLEHS 281  
 Sequence 359 AA;

RESULT 24

Query Match 100.0%; Score 99; DB 7; Length 359; PR XX  
 Best local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQOLFLEHS 18  
 Db 264 SSDGLWNNTQOLFLEHS 281  
 Sequence 359 AA;

PR Key Location/Qualifiers  
 PR Misc-difference 123 /note= "encoded by GAG"  
 PR Misc-difference 161 /note= "encoded by GACT"  
 PR Misc-difference 201 /note= "encoded by ACAGT"

XX WO2003002722-A2.  
 XX 09-JAN-2003.  
 XX PR 01-JUL-2002; 2002WO-US020890.  
 XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX PT McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;  
 XX DR N-PSDB; ABZ63336.  
 XX WPI; 2003-210268/20.  
 XX DR N-PSDB; ABZ63336.  
 XX PT New nucleic acid comprising a mammalian T cell Immunoglobulin domain and mucin domain gene sequences, useful for treating cancer or asthma, allergy, eczema or autoimmune disease.  
 XX PT New nucleic acid comprising a mammalian T cell Immunoglobulin domain and mucin domain gene sequences, useful for treating cancer or asthma, allergy, eczema or autoimmune disease.  
 XX PS Claim 10; Page 87-88; 94pp; English.  
 XX CC The present sequence is a human T cell immunoglobulin domain and mucin domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2, TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with conserved IgV and mucin domains. The locus comprising the TIM family is genetically associated with immune dysfunction, including asthma. The TIM gene family is located within a region of human chromosome 5 that is commonly deleted in malignancies and myelodysplastic syndrome. Variants of TIM-1 and TIM-3 are associated with susceptibility to airway hyperreactivity and protection against these responses. T cells express TIM proteins, which critically regulate CD4 T cell differentiation. TIM cells associated with protection against these responses. T cells express TIM-1. TIM polypeptides and polynucleotides are useful for treating cancer, asthma, allergies, eczema or autoimmune diseases.  
 CC Of TIM-1 and TIM-3 are associated with susceptibility to airway hyperreactivity and allergic T cell responses, and other variants associated with protection against these responses. T cells express TIM proteins, which critically regulate CD4 T cell differentiation. TIM cells preferentially express TIM-3, while Th2 cells preferentially express TIM-1. TIM polypeptides and polynucleotides are useful for treating cancer, asthma, allergies, eczema or autoimmune diseases.  
 CC Commonly deleted in malignancies and myelodysplastic syndrome. Variants of TIM-1 and TIM-3 are associated with susceptibility to airway hyperreactivity and protection against these responses. T cells express TIM proteins, which critically regulate CD4 T cell differentiation. TIM cells associated with protection against these responses. T cells express TIM-1. TIM polypeptides and polynucleotides are useful for treating cancer, asthma, allergies, eczema or autoimmune diseases.  
 XX SQ Sequence 364 AA;

Query Match	100.0%	Score	99	DB	6	Length	364
Best Local Similarity	100.0%	Pred.	No	1.2e-06			
Matches	18						
Conservative	0						
Mismatches	0						
Indels	0						
Gaps	0						

Qy 1 SSDGLWNNTQFLERS 18  
 Db 269 SSDGLWNNTQFLERS 286

RESULT 19

ID ABP70442  
 ID ABP70442 standard; protein; 364 AA.  
 AC ABP70440;  
 DT 22-APR-2003 (first entry)

DE Amino acid sequence of human TIM-1 allele 3.

XX T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3; TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema; myelodysplastic syndrome; airway hyperreactivity; cancer; asthma; allergic T cell response; autoimmune disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 208 /note= "encoded by RCG"

XX PN WO2003002722-A2.

XX PD 09-JAN-2003.

XX PR 01-JUL-2002; 2002WO-US020890.

XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.

XX PI McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;

XX DR WPI; 2003-210268/20.



CC in large amounts by expression of the nucleic acid in prokaryotic or eukaryotic host cells or in transgenic animals. It can be used in the detection, prevention and treatment of HAV infection, in methods of purifying or removing HAV from samples, and methods of determining the anti-HAV activity of caps. Expression in transgenic animals provides a method for testing vaccine efficacy

XX SQ Sequence 451 AA;

Query Match 84.8%; Score 84; DB 2; Length 451;  
Best Local Similarity 88.9%; Pred. No. 0.00028; Mismatches 2; Indels 0; Gaps 0;  
Matches 16; Conservative 0; MisMatches 2; Pred. No. 0.00028; Indels 0; Gaps 0;

Qy 1 SDGGLWNNNOTQLEHS 18  
Db 344 SDGGLWNNNOTQLEHS 361

RESULT 23  
AAQ26686  
ID AAO26686 standard; peptide; 18 AA.  
XX  
AC AAC26686;  
XX  
DT 20-MAR-2003 (first entry)  
XX Human KIM-1 mucin domain related peptide, SEQ ID No 14.  
XX  
KW Cyrostatic; gene therapy; antibody; antigen; antigen-binding;  
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;  
KW renal disease; injury; renal cancer.  
XX OS Synthetic.  
PN WO2002029920-A1.  
XX PD 12-DEC-2002.  
XX PR 01-JUN-2001; 2001US-0255907P.  
XX PR 04-JUN-2001; 2001US-0255907P.  
XX PA (BIOJ ) BIOPHARM INC.  
PA (GENO ) GEN HOSPITAL CORP.  
XX PI Bailly V, Bonventre J;  
XX PS Disclosure; Fig 1A; 42pp; English.

XX The invention relates to a novel antibody, antibody derivative or antigen -binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 polypeptide, useful for treating or preventing renal disease or injury, e.g. renal cancer.

XX DR WPI, 2003-156845/15.

XX PT New antibody, antibody derivative or antigen-binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 polypeptide, useful for treating or preventing renal disease or injury, e.g. renal cancer.

XX PS Disclosure; Fig 1A; 42pp; English.

XX The invention relates to a novel antibody, antibody derivative or antigen -binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells. The antibody, antibody derivative or antigen-binding polypeptide is useful for treating or preventing renal disease or injury, e.g. renal cancer. The antibody is also useful for inhibiting shedding of the KIM-1 polypeptide. This sequence represents a human KIM-1 mucin domain related peptide of the invention

XX SQ Sequence 18 AA;

Query Match 53.5%; Score 53; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; MisMatches 0; Pred. No. 0.45; Indels 0; Gaps 0;

Qy 1 SDSGLWNNNOTQLEHS 16  
Db 489 SLIDLWNNNQOMFWIQ 504

RESULT 25  
AAQ26686

Db 10 SSDGLWNNN 18

RESULT 24  
AAE18306 standard; protein; 981 AA.  
AC AAE18306;  
XX DE 07-MAY-2002 (first entry)  
XX Venezuelan equine encephalitis virus (VEE) glycoprotein V3014.  
XX KW Venezuelan equine encephalitis virus; VEE; vaccine; HIV infection;  
KW human immunodeficiency virus; alpha-virus replicon; immune response;  
KW therapy; glycoprotein V3014.  
XX OS Venezuelan equine encephalitis virus.  
XX PN WO200203917-A2.  
XX PD 17-JAN-2002.  
XX PF 09-JUL-2001; 2001WO-US021701.  
XX PR 07-JUL-2000; 2000US-0216995P.  
XX PA (ALPH-) ALPHAVAX INC.  
PA (UVMC-) UNIV NORTH CAROLINA.  
XX Olmsted R, Keith P, Dryga S, Caley I, Maughan M, Johnston R;  
PI Davis N, Swanstrom R;  
XX DR WPI; 2002-171664/22.  
DR N-PSDB; AAD25138.  
XX PT Composition useful for treating or preventing HIV infections, comprises two or more isolated nucleic acids encoding env, gag or pol gene product of HIV or immunogenic fragment of the gene products.  
XX PS Example 4; Page 180-183; 201PP; English.

XX The invention relates to a composition comprising isolated nucleic acids encoding env, gag or pol gene product of human immunodeficiency virus or immunogenic fragment of the gene products. The gag gene product is modified to inhibit formation of virus-like particles containing gag gene product and their release from cells, and the pol gene product is modified to inhibit reverse transcriptase activity. The invention also relates to a method for producing an alpha-virus replicon particle used in vaccines. The composition is useful for inducing an immune response to human immunodeficiency virus (HIV) or for treating or preventing HIV infection in a subject. The alpha-virus replicon particle is useful in a vaccine. The composition is useful for administering a protein or peptide to a subject. A composition comprising an alpha-virus replicon particle and as a virus replicon particle is useful as a clinical trial material and as a commercial product. The present sequence is Venezuelan equine encephalitis virus (VEE) glycoprotein V3014 used in the exemplification of the invention.

XX SQ Sequence 981 AA;

Query Match 48.5%; Score 48; DB 5; Length 981;  
Best Local Similarity 50.0%; Pred. No. 1.8e+02; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGLWNNNOTQLEHS 16  
Db 489 SLIDLWNNNQOMFWIQ 504

RESULT 25

ID AAO26688 standard; peptide; 18 AA.  
 XX  
 AC AAO26688;  
 XX  
 DT 20-MAR-2003 (first entry)  
 XX  
 DB Human KIM-1 mucin domain related peptide, SEQ ID No 16.  
 XX  
 KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;  
 KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;  
 KW renal disease; injury; renal cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO20029920-A1.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PP 31-MAY-2002; 2002WO-US017402.  
 XX  
 PR 01-JUN-2001; 2001US-0295449P.  
 PR 04-JUN-2001; 2001US-0295907P.  
 XX  
 PA (BIO) ) BIOPHARMA INC.  
 PA (GENO ) GEN HOSPITAL CORP.  
 XX  
 PI Bailly V, Bonventre J;  
 XX  
 DR WPI; 2003-156845/15.  
 PT New antibody, antibody derivative or antigen-binding polypeptide that  
 PT inhibits proteolytic release of a soluble kidney injury molecule-1  
 PT polypeptide, useful for treating or preventing renal disease or injury,  
 PT e.g. renal cancer.  
 XX  
 PS Disclosure; FIG 1A; 42pp; English.  
 XX  
 CC The invention relates to a novel antibody, antibody derivative or antigen  
 CC -binding polypeptide that inhibits proteolytic release of a soluble  
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.  
 CC The antibody, antibody derivative or antigen-binding polypeptide is  
 CC useful for treating or preventing renal disease or injury, e.g. renal  
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1  
 CC polypeptide. This sequence represents a human KIM-1 mucin domain related  
 CC peptide of the invention  
 XX  
 SQ Sequence 18 AA;

Query Match 45.5%; Score 46; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QTOQFLEHS 18  
 Db 1 QTQFLEHS 9

RESULT 26

ID ABC93049  
 ID ABC93049 standard; protein; 508 AA.  
 XX  
 AC ABC93049;  
 XX  
 DT 21-NOV-2002 (first entry)  
 XX  
 DE S. cerevisiae BAX-associated protein fragment SEQ ID 56.  
 XX  
 KW Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;  
 KW vasoconstrictor; vaccine; gene therapy; proliferative disorder; cancer;  
 KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;  
 KW neurodegeneration; cell death.  
 XX  
 OS Saccharomyces cerevisiae.

---

XX  
 PN WO200264766-A2.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PP 21-DEC-2001; 2001WO-EP015398.  
 XX  
 PR 22-DEC-2000; 2000EP-00870318.  
 PR 04-JAN-2001; 2001EP-00870002.  
 PR 09-JAN-2001; 2001EP-00870003.  
 XX  
 PA (JAN) ) JANSSEN PHARM NV.  
 XX  
 PI Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;  
 XX  
 DR WPI; 2003-667002/71.  
 DR N-PSDB; ABQ76315.  
 XX  
 PT New isolated nucleic acid representing a synthetic Bax-gene, useful as  
 PT medicament for treating, preventing and/or alleviating yeast or fungal  
 PT infections or proliferative disorders, or for preventing apoptosis in  
 PT certain diseases.  
 XX  
 PS Claim 36; FIG 1; 344pp; English.  
 XX  
 CC This invention describes a novel nucleic acid representing a synthetic  
 CC Bax gene. The Bax gene of the invention is useful for identifying Bax-  
 CC resistant yeast or fungi, identifying, or obtaining and identifying  
 CC Candida spp. sequences that are differentially expressed in a pathway  
 CC eventually leading to programmed cell death or identifying inhibitors or  
 CC inhibitor sequences of Bax-induced cell death. The products of the  
 CC invention have cytostatic, fungicide, immunosuppressive, virucide and  
 CC vasotropin activity and can be used in vaccines or for gene therapy. The  
 CC isolated nucleic acids, polypeptides, pharmaceutical compositions,  
 CC antisense molecules and antibodies are useful as medicaments or in  
 CC preparing a medicament for treating, preventing and/or alleviating  
 CC diseases associated with yeast or fungi or proliferative disorders, such  
 CC as cancer, or for preventing apoptosis in certain diseases. The compounds  
 CC or polypeptides, or the genetically modified organism are useful for  
 CC preparing a medicament for modifying the endogenous flora of humans and  
 CC other mammals. The vaccine is useful for immunizing against yeast or  
 CC fungal infections. Apoptosis-related diseases include autoimmune disease,  
 CC ischaemia, diseases related with viral infections or neurodegenerations.  
 CC This sequence represents a polypeptide associated with the Bax gene  
 CC described in the disclosure of the invention  
 XX  
 SQ Sequence 508 AA;

Query Match 45.5%; Score 46; DB 5; Length 508;  
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 WNNNNTQFILE 16  
 Db 160 WNNNNTQFILE 170

RESULT 27

ID ABR52836  
 ID ABR52836 standard; protein; 508 AA.  
 XX  
 AC ABR52836;  
 XX  
 DT 20-JUN-2003 (first entry)  
 XX  
 DE Protein sequence #SEQ ID 537.  
 XX  
 KW Multiprotein complex; eukaryote; drug target; diagnosis.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN EP1258494-A1.

PD 20-NOV-2002.  
 XX  
 PF 20-DEC-2001; 2001EP-00130253.  
 XX  
 PR 15-MAY-2001; 2001EP-00111774.  
 PT (CELL-) CELLZONE AG.  
 PA DR N-PSDB; ACC60878.  
 XX  
 PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;  
 XX  
 DR WPI; 2003-250078/25.  
 XX  
 PT New isolated protein complexes useful for diagnosing a disease or  
 PT disorder, or as a target for an active agent of a pharmaceutical,  
 PT preferably a drug target in the treatment or prevention of disease or  
 PT disorder.  
 XX  
 PS Disclosure; SEQ ID NO 537; 17pp + Sequence Listing; English.  
 XX  
 CC The invention relates to multiprotein complexes from eukaryotes. Proteins  
 CC of the invention and DNA sequences encoding them are given in records  
 ABG5260-ABR3903 and ACC60810-ACG6194 respectively. The complexes are  
 CC obtainable by using a protein as a bait and isolating the set of proteins  
 CC which is attached thereto from cells. Such protein complexes may comprise  
 up to 30 distinct proteins. Protein complexes of the invention are useful  
 CC for diagnosing a disease or disorder, or as a target for an active agent  
 CC of a pharmaceutical, preferably a drug target in the treatment or  
 prevention of a disease or disorder. Note: The sequence data for this  
 CC patent is not represented in the printed specification, but is based on  
 CC sequence information supplied by the European Patent Office. The complete  
 CC document is available on CD-ROM  
 XX  
 SQ Sequence 508 AA;

Query Match 46.5%; Score 46; DB 6; Length 508;  
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 6 WNNNOTQFLF 16  
 Db 160 WNNNASMFILE 170

RESULT 28  
 ADKG2270  
 ID ADKG2270 standard; protein; 508 AA.  
 XX  
 AC ADKG2270;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Disease treating protein complex-derived protein #261.  
 XX  
 KW protein complex; drug target; diagnosis.  
 XX  
 OS Unidentified.  
 XX  
 PN EP1338608-A2.  
 XX  
 PD 27-AUG-2003.  
 XX  
 PP 20-DEC-2002; 2002EP-00102902.  
 XX  
 PR 20-DEC-2001; 2001EP-00130253.  
 XX  
 PA (CELL-) CELLZONE AG.

Query Match 46.5%; Score 46; DB 6; Length 508;  
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 6 WNNNOTQFLF 16  
 Db 160 WNNNASMFILE 170

RESULT 29  
 ABG71366  
 ID ABG71366  
 AC ABG71366;  
 XX  
 DT 28-JAN-2003 (first entry)  
 XX  
 DE Potato plastidic targeted beta-amylase (ppt-beta-amylase).  
 KW Potato; starch degrading enzyme; enzyme; starch degradation;  
 KW washing agent; flushing agent; potato plastidic targeted beta-amylase;  
 KW ppt-beta-amylase.  
 XX  
 OS Solanum tuberosum.  
 PN WO2002086112-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PP 25-APR-2002; 2002WO-EP004609.  
 XX  
 PR 25-APR-2001; 2001EP-0011005.  
 XX  
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Scheidig A, Kossmann J, Froehlich A;  
 XX  
 DR WPI; 2003-058726/05.  
 DR N-PSDB; ABS56813.  
 XX  
 PT Novel nucleic acid useful for modifying starch degradation and as  
 hybridization probes to isolate related genes, encodes enzyme involved in

PS Claim 1; Page 105-107; 107pp; English.

The invention relates to a nucleic acid molecule encoding a starch degrading enzyme. The nucleic acid is useful for reducing endogenous activity of a biologically active fragment, for modifying starch degradation, as a hybridization probe to isolate related genes and as a primer for amplification techniques such as polymerase chain reaction. The nucleic acid is also useful as an agent for starch degradation in a washing or flushing agent. This sequence represents a potato plastidic targeted beta-amylase (pp-beta-amylase) polypeptide

SQ Sequence 545 AA;

	Query Match	Score	DB	Length
Best Local Similarity	46.5%	46	6	545
Matches	8	2e-02		
Conservative	57.1%	Pred. No.		
		Mismatches	1	
		Indels	5	
Ov	3	DGJWNNTNOTLIE	16	
Db	324	DGTWNSEYGOFFLE	337	

RESULT 30

ID ADJ49214  
 ID ADJ49214 standard; protein; 545 AA.

XX AC ADJ49214;

XX DT 06-MAY-2004 (first entry)

XX DB Oil-associated gene related protein #714.

XX KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.

XX OS Unidentified.

XX PN US2004025202-A1.

XX PP 05-FEB-2004.

XX PR 14-MAR-2003; 2003US-00389566.

XX PR 15-MAR-2002; 2002US-0165301P.

PR 26-JUN-2002; 2002US-0391788P.

PR 26-JUN-2002; 2002US-0392018P.

PA (LAUR/) LAURIE C C.

PA (RAVAN/) RAVANELLO M.

PA (SAV/) SAVAGE T.

PA (LEDE/) LEDEAUX J R.

PA (ROGE/) ROGERS J A.

XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;

XX DR WPI; 2004-142683/14.

PT Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic plant seed.

PS Example 3; SEQ ID NO 1218; 22pp; English.

CC The invention relates to a recombinant DNA construct comprising a CC promoter functional in plants operably linked to an oil-associated gene. CC The construct is useful for transgenic plant seed which has in its genome CC the construct, that is functional in the plant to transcribe the oil- associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for CC producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents the amino acid CC sequence of an oil-associated gene related protein.

SQ	Sequence	545 AA:	XX
Query	Match	46.5%; Score 46;	DB 8; Length 545;
Best	Local Similarity	57.1%; Pred. No. 2e-02;	
Matches	8; Conservative	1; Mismatches 5; Indels 0; Gaps 0;	
Qy	3 DGLWNWNQQTQPLE	16	
Db	324 DGTWNISBYGQFPLE	337	
RESULT	31		
ID	ABR57094		
ID	ABR57094 standard; peptide; 114 AA.		
XX			
AC	ABR57094;		
XX			
DT	26-AUG-2003	(First entry)	
XX			
DE	MHLR comparison related RAHEPLBC2 amino acid sequence.		
XX			
KW	LHR; MHLR; immunoglobulin; Ig; immunoglobulin heavy chain dimer; ligand-combined partner; cell surface adhesion molecule; ligand; lymphocyte cell surface glycoprotein.		
XX			
OS	Unidentified.		
XX			
PN	JP2002325589-A.		
XX			
PD	12-NOV-2002.		
XX			
PF	21-NOV-1990; 2002JP-00026825.		
XX			
PR	22-NOV-1999; 89US-00444625.		
PR	21-NOV-1990; 91JP-00501520.		
XX			
PA	(GETH ) GENENTECH INC.		
XX			
DR	WPI; 2003-407283/39.		
XX			
CC	A fused protein consisting of a ligand-combined protein and a stable plasma protein, a polypeptide, a nucleic acid, a replicable expression vector, a composition.		
PT			
XX			
PS	Example 1; Fig 11; 44pp; Japanese.		
XX			
CC	The present invention describes a polypeptide (1) containing an immunoglobulin (Ig) heavy chain dimer having no Ig light chain in which the amino acid sequence of a ligand-combined partner is a receptor, a carrier protein, a hormone, a growth factor, an enzyme or a nutritive substance, but is not a subunit polypeptide encoded by a lymphocyte inducing receptor, an Ig gene super family-containing element, a protein homologous to it, or a separated gene substitute of the variable region of at least one Ig heavy chain. Its combined partner is fused with the amino acid sequence of an Ig stationary region at its C-end and maintains its combining feature. Also described: (1) a nucleic acid encoding (1); (2) a replicable expression vector containing the nucleic acid or (1); (3) a composition containing cells transformed by the expression vector of (2); and (4) producing (1), comprising culturing the cells of (3) in which the transformed cells are cultured and the polypeptide is recovered from the cell culture. The polypeptide is useful as a cell surface adhesion molecule and a ligand. In an example from the present invention mouse lymphocyte cell surface glycoprotein designated LHR (MHLR) was isolated from a mouse spleen and purified and cloned. The present sequence represents an amino acid sequence given in comparison with an MHLR amino acid sequence, which is used in an example from the present invention.		
CC			
CC	Sequence 114 AA;		
XX			

Matches	8;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	2	SDGLWNNGTQ	12						
		:							
Db	97	SDGLWNNDNFQ	107						
RESULT	32								
ABR57095									
ID	ABR57095	standard; peptide; 114 AA.							
XX									
AC	ABR57095;								
XX									
DT	26-AUG-2003	(first entry)							
XX									
DB	MLHR comparison related RA.ASGREC amino acid sequence.								
XX									
KW	LHR; MLHR; immunoglobulin; Ig; immunoglobulin heavy chain dimer; ligand; lymphocyte cell surface glycoprotein.								
XX									
OS	Unidentified.								
XX									
PN	JP2002325589-A.								
XX									
PD	12-NOV-2002.								
XX									
PF	21-NOV-1990; 2002UP-00026825.								
XX									
PR	22-NOV-1989; 89US-00444625.								
XX									
PR	21-NOV-1990; 91UP-00501520.								
XX									
PA	(GETH ) GENENTECH INC.								
XX									
DR	WPI; 2003-407283/39.								
XX									
PT	A fused protein consisting of a ligand-combined protein and a stable plasma protein, a polypeptide, a nucleic acid, a replicable expression vector, a composition,								
PT	Example 1; Fig 11; 44pp; Japanese.								
XX									
CC	The present invention describes a polypeptide (1) containing an immunoglobulin (Ig) heavy chain dimer having no Ig light chain in which the amino acid sequence of a ligand-combined partner is a receptor, a carrier protein, a hormone, a growth factor, an enzyme or a nutritive substance, but is not a subunit polypeptide encoded by a lymphocyte inducing receptor, an Ig gene super family constituting element, a protein homologous to it, or a separated gene substitute of the variable region of at least one Ig heavy chain. Its combined partner is fused with the amino acid sequence of an Ig stationary region at its C-end and maintains its combining feature. Also described: (1) a nucleic acid encoding (1); (2) a replicable expression vector containing the nucleic acid of (1); (3) a composition containing cells transformed by the expression vector of (2); and (4) producing (1), comprising culturing the cells of (3) in which the transformed cells are cultured and the polypeptide is recovered from the cell culture. The polypeptide is useful as a cell surface adhesion molecule and a ligand. In an example from the present invention mouse lymphocyte cell surface glycoprotein designated LHR (MLHR) was isolated from a mouse spleen and purified and cloned. The present sequence represents an amino acid sequence given in comparison with an MLHR amino acid sequence, which is used in an example from the present invention								
XX	Sequence 114 AA;								
Query Match	45.5%; Score 45; DB 6; Length 114;								
Best local Similarity	72.7%; Pred. No. 53;								
Matches	8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;								
Qy	2 SDGLWNNGTQ 12								
Db	97 SDGLWNNDNFQ 107								
Query Match	45.5%; Score 45; DB 4; Length 244;								
Best local Similarity	47.4%; Pred. No. 1.2e+02;								
Matches	9; Conservative 3; Mismatches 3; Indels 4; Gaps 1;								
SQ	Sequence 244 AA;								

Query Match

Best local Similarity

Matches

Qy

Db

Query Match

Best local Similarity

Matches

Qy

Db

RESULT 34	3	DGLWNNNQ---TQLLEH	17
AAM42108	ID	AAM42108	standard; protein; 244 AA.
XX	AC		
AAM42108;			
XX	DT		
22-OCT-2001	(first entry)		
XX	DE	Human polypeptide SEQ ID NO 7039.	
XX	KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemoattractant; thromolytic; drug screening; arthritis; inflammation; leukaemia.	
XX	KW		
OS	Homo sapiens.		
XX	PN	WO200153312-A1.	
XX	PD		
XX	PR	26-JUL-2001.	
XX	PR	23-DEC-1999; 99US-00471275.	
PR	PR	21-JAN-2000; 2000US-00488725.	
PR	PR	25-APR-2000; 2000US-0052317.	
PR	PR	20-JUN-2000; 2000US-0058042.	
PR	PR	19-JUL-2000; 2000US-00620312.	
PR	PR	03-AUG-2000; 2000US-00633450.	
PR	PR	14-SEP-2000; 2000US-00662191.	
PR	PR	19-OCT-2000; 2000US-00693036.	
PR	PR	29-NOV-2000; 2000US-00727344.	
XX	PA	(HYSE-1) HYSEQ INC.	
XX	PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA	
PI	PI	Zhou P, Goodrich R, Dumanac RT;	
XX	DR	WPI; 2001-442253/47.	
DR	N-PSSDB;	AAI61264.	
XX	PT	Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.	
XX	PS	Example 2; SEQ ID NO 7039; 10078P; English.	
XX	CC	The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42113) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or poly nucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification.	
XX	CC		
CC	CC		
SQ	Sequence 244 MA;		

Best Local Similarity 47.4%; Pred. No. 1.2e+02; Matches 9; Conservative 3; Mismatches 3; Indels 4; Gaps 1; Qy	
3	DGLWNINQ---TQFLLEH 17
Db	81 DGTWNNDNQLOEMAQLRIKH 99
RESULT 35	
RAY9671	
ID AAY9671 standard; protein; 265 AA.	
XX	
XX AAY9671;	
XX	
DT 03-NOV-2000 (first entry)	
XX	
DB Human GTPase associated protein-22.	
XX	
KW Guanine nucleotide binding protein; GTP-binding protein; G-protein; GTPase; GTPase associated protein; GTPAP; cell proliferation; autoimmune; inflammatory; immune system disorder; cancer; AIDS; acquired immune deficiency syndrome; asthma; atherosclerosis; arthritis; systemic lupus erythematosus; psoriasis; human.	
KW	
XX OS Homo sapiens.	
XX	
PN WO20031263-A2.	
XX	
PD 02-JUN-2000.	
XX	
PP 23-NOV-1999; 99W0-US0288013.	
XX	
PR 23-NOV-1998; 98US-0109592P.	
PR 04-FEB-1999; 99US-0118610P.	
PR 06-APR-1999; 99US-0127990P.	
XX PA (INCY-) INCYTE PHARM INC.	
XX PI Hillman JL, Tang YT, Bandman O, Lal P, Yue H, Lu DAM, Baughn MR;	
XX PI Yang J, Azimai Y;	
XX DR WPI; 2000-400073/34.	
DR N-PSB; AAA49192.	
PT Human GTPase associated proteins, polynucleotides, and antibodies, useful for diagnosing, preventing and treating various diseases such as atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS), asthma, and autoimmune diseases.	
PT	
PT	
PS Claim 1; Page 108-109; 144pp; English.	
XX	
CC Human cDNA libraries from various tissues were screened for GTPase associated proteins (GTPAP). The present sequence is human GTPAP-22 protein. This sequence was derived from a cDNA library of the HNT2 cell line from a human teratocarcinoma. This protein is expressed in nervous, gastrointestinal and cardiovascular tissue. The GTPAP proteins may be used to define agonists and antagonists of GTPAP activity and to generate antibodies to GTPAP. This means the GTPAP proteins may be useful for treatment or prevention of diseases associated with GTPAP such as cell proliferation disorders, autoimmune disorders, inflammatory disorders, immune system disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic lupus erythematosus and psoriasis	
CC	
CC	
SQ Sequence 265 AA;	
XX	

RESULT 36

ADD46355  
ID ADD46355 standard; protein; 301 AA.  
XX AC

XX DT 29-JAN-2004 (first entry)  
XX DE Rat Protein P08290, SEQ ID NO 12033.  
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX OS Rattus norvegicus.  
XX PN WO2003016475-A2.  
XX PD 27-FEB-2003.  
XX PP 14-AUG-2002; 2002WO-US025765.  
XX PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX PA (GERHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX PI Woolf C, D'urso D, Befort K, Costigan M;  
XX DR WPI; 2003-268312/26.  
DR GENBANK; P08290.  
XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.  
XX PS Claim 1; Page: 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification), which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 301 AA;

Query Match 45.5%; Score 45; DB 7; Length 301;  
Best local Similarity 72.7%; Pred. No. 1; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 1; Sequence 301 AA;

QY 2 SDGLWNNNQTO 12

Db 276 SDGLWNNNQTO 286

RESULT 37

ADD63357  
ID ADE63357 standard; protein; 301 AA.  
XX AC

XX DT 29-JAN-2004 (first entry)  
XX DE Rat Protein P08290, SEQ ID NO 9295.  
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX OS Rattus norvegicus.  
XX PR 14-AUG-2002; 2002WO-US025765.  
XX PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX PA (GERHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX PI Woolf C, D'urso D, Befort K, Costigan M;  
XX DR WPI; 2003-268312/26.  
DR GENBANK; P08290.  
XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.  
XX PS Claim 1; Page: 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification), which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 301 AA;

Query Match 45.5%; Score 45; DB 7; length 301;  
 Best Local Similarity 72.7%; Pred. No. 1.5e+02; Length 301;  
 Matches 8; Conservative 1; Mismatches 4+02; Indels 0; Gaps 0;

Qy 2 SDGLWNNNNQO 12  
 Db 276 SDGLWNNDNFCCQ 286

RESULT 38

AAB92470 AAB92470 standard; protein; 309 AA.

XX ID AAB92470;

AC XX AAB92470;

DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:10536.

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX OS Homo sapiens.

PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PP 28-JUL-2000; 2000EP-00116126.

XX PR 29-JUL-1999; 99JEP-00248036.

PR 27-AUG-1999; 99JEP-00300253.

PR 11-JAN-2000; 2000EP-00118776.

PR 02-MAY-2000; 2000EP-00183767.

PR 09-JUN-2000; 2000EP-00241899.

XX PA (HELI-) HELIX RES INST.

XX PT Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PT Iishi S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX DR Primer sets for synthesizing Polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX PS Claim 8; SEQ ID NO 10536; 253pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH1366 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; ARB92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX Sequence 309 AA;

RESULT 39

ABB97591 ABB97591 standard; protein; 309 AA.

XX ID ABB97591;

AC XX ABB97591;

DT 27-JUN-2002 (first entry)

DE Novel human protein SEQ ID NO: 859.

XX Human; antianemic; vulnary; antiinflammatory; immunomodulator; antinfertility; cerebroprotective; cyrostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST; expressed sequence tag.

XX OS Homo sapiens.

XX PN WO200222660-A2.

XX PD 21-MAR-2002.

XX PP 10-SEP-2001; 2001WO-US026015.

XX PR 11-SEP-2000; 2000US-00659671.

XX PA (HYSEB-) HYSEQ INC.

XX PT Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

PT PI Xie AJ, Yang Y, Wehrman T, Drmanac RT;

XX DR WPI; 2002-292408/33.

DR N-PDB; ABN32777.

XX An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.

XX PS Claim 20; SEQ ID NO 859; 509pp; English.

XX The present invention provides the protein and coding sequences of novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haemopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activation or inhibition e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention.

XX Sequence 309 AA;

Query Match 45.5%; Score 45; DB 5; Length 309;  
 Best Local Similarity 47.4%; Pred. No. 1.5e+02; Length 309;  
 Matches 9; Conservative 3; Mismatches 4+02; Indels 4; Gaps 1;

Qy 3 DGLWNNNQ---TOLFLEH 17  
 Db 74 DGTWNNDNQLOEMAQLRIKH 92

RESULT 40

AAW0322 AAW0322 standard; protein; 511 AA.

SQ ID

Search completed: December 30, 2004, 16:10:01  
 Job time : 165 sec

XX  
 AC AAM40322;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 3467.  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000MQ-US034263.  
 XX  
 PR 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00488725.  
 PR 25-APR-2000; 2000US-0052317.  
 PR 20-JUN-2000; 2000US-00598042.  
 PR 19-JUL-2000; 2000US-00620312.  
 PR 03-AUG-2000; 2000US-0053450.  
 PR 14-SEP-2000; 2000US-0062191.  
 PR 19-OCT-2000; 2000US-0063036.  
 PR 29-NOV-2000; 2000US-00727344.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 XX  
 PT Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
 XX  
 PR Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI: 2001-442253/47.  
 DR N-PSDB; AA159478.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.  
 XX  
 PS Example 6; SEQ ID NO 3467; 10078pp; English.  
 XX  
 CC The invention relates to human nucleic acids (AA157798-AA161369) and the  
 CC encoded polypeptides (AAM3862-AAM4223) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukemias and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification.  
 XX  
 SQ Sequence 511 AA;

Query Match 45.5%; Score 45; DB 4; Length 511;  
 Best Local Similarity 47.4%; Pred No. 2.6e-02;  
 Matches 9; Conservative 3; Mismatches 3; Indels 4; Gaps 1;

QY 3 DGLWNWNO---TQPLEH 17  
 Db 74 DGTWNNDNQLOBMAQLRIKH 92

GenCore version 5.1.6  
copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model  
Run on: December 30, 2004, 16:13:23 ; Search time 143 Seconds  
(without alignments)

45.280 Million cell updates/sec  
Title: US-10-718-321-1  
Perfect score: 99  
Sequence: 1 SSDGLIANNNOTQFLFHS 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues  
Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 150 summaries

Database : Published Applications AA:\*

1: /cgtr2\_6/ptodata/1/pubpa/US07\_PUBCOMB.pep: \*  
2: /cgtr2\_6/ptodata/1/pubpa/PCT\_NEW\_PUB\_pep: \*  
3: /cgtr2\_6/ptodata/1/pubpa/US06\_NEW\_PUB\_pep: \*  
4: /cgtr2\_6/ptodata/1/pubpa/US06\_PUBCOMB.pep: \*  
5: /cgtr2\_6/ptodata/1/pubpa/US07\_NEW\_PUB\_pep: \*  
6: /cgtr2\_6/ptodata/1/pubpa/PCTNS\_PUBCOMB.pep: \*  
7: /cgtr2\_6/ptodata/1/pubpa/US08\_NEW\_PUB\_pep: \*  
8: /cgtr2\_6/ptodata/1/pubpa/US08\_PUBCOMB.pep: \*  
9: /cgtr2\_6/ptodata/1/pubpa/US09\_PUBCOMB.pep: \*  
10: /cgtr2\_6/ptodata/1/pubpa/US09B\_PUBCOMB.pep: \*  
11: /cgtr2\_6/ptodata/1/pubpa/US07\_NEW\_PUB\_pep: \*  
12: /cgtr2\_6/ptodata/1/pubpa/US09\_NEW\_PUB\_pep: \*  
13: /cgtr2\_6/ptodata/1/pubpa/US10\_PUBCOMB.pep: \*  
14: /cgtr2\_6/ptodata/1/pubpa/US10\_PUBCOMB.pep: \*  
15: /cgtr2\_6/ptodata/1/pubpa/US10C\_PUBCOMB.pep: \*  
16: /cgtr2\_6/ptodata/1/pubpa/US10D\_PUBCOMB.pep: \*  
17: /cgtr2\_6/ptodata/1/pubpa/US10\_NEW\_PUB\_pep: \*  
18: /cgtr2\_6/ptodata/1/pubpa/US11\_NEW\_PUB\_pep: \*  
19: /cgtr2\_6/ptodata/1/pubpa/US10\_PUBCOMB.pep: \*  
20: /cgtr2\_6/ptodata/1/pubpa/US10\_PUBCOMB.pep: \*

Pred. No. 16 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match length	DB ID	Description
1	99	100.0	359	14 US-10-188-012-17 Sequence 17, App1
2	99	100.0	359	14 US-10-188-012-19 Sequence 19, App1
3	99	100.0	359	14 US-10-295-027-302 Sequence 302, App1
4	99	100.0	359	15 US-10-188-032-64 Sequence 64, App1
5	99	100.0	364	14 US-10-188-012-25 Sequence 25, App1
6	99	100.0	364	14 US-10-188-012-27 Sequence 27, App1
7	99	100.0	365	14 US-10-188-012-21 Sequence 21, App1
8	94	94.9	359	14 US-10-188-012-23 Sequence 23, App1
9	48	48.5	981	9 US-09-991-258-13 Sequence 13, App1
10	47	47.5	102	15 US-10-424-599-175126 Sequence 175126, App1
11	46	46.5	508	14 US-10-369-493-1469 Sequence 1469, App1
12	46	46.5	16	US-10-451-67A-56 Sequence 56, App1
13	46	46.5	545	15 US-10-389-566-1218 Sequence 1218, App1

#### SUMMARIES

Summary No.	Score	Query Match length	DB ID	Description
1	99	100.0	359	14 US-10-437-963-16357 Sequence 163657, Sequence 163658, Sequence 163659, Sequence 9340, App1
2	99	100.0	359	14 US-10-437-963-16358 Sequence 9341, App1
3	99	100.0	359	14 US-10-437-963-16351 Sequence 49522, A
4	99	100.0	359	14 US-10-437-963-16351 Sequence 15, App1
5	99	100.0	359	14 US-10-437-963-16352 Sequence 1, App1
6	99	100.0	359	14 US-10-437-963-16352 Sequence 15, App1
7	99	100.0	359	14 US-10-437-963-16352 Sequence 15, App1
8	99	100.0	359	14 US-10-437-963-16352 Sequence 15, App1
9	94	94.9	359	14 US-10-437-963-16352 Sequence 15, App1
10	47	47.5	102	15 US-10-437-963-16352 Sequence 15, App1
11	46	46.5	508	14 US-10-437-963-16352 Sequence 15, App1
12	46	46.5	16	US-10-437-963-16352 Sequence 15, App1
13	46	46.5	545	15 US-10-437-963-16352 Sequence 15, App1
14	45.5	45.5	1464	15 US-10-437-963-16357 Sequence 163657, Sequence 163658, Sequence 163659, Sequence 9340, App1
15	45.5	46.0	770	16 US-10-437-963-16358 Sequence 9341, App1
16	45	45.5	273	14 US-10-437-963-16351 Sequence 49522, A
17	45	45.5	687	15 US-10-437-963-16352 Sequence 15, App1
18	45	45.5	1464	10 US-09-934-070-15 Sequence 1, App1
19	45	45.5	1464	10 US-09-932-011-1 Sequence 1, App1
20	45	45.5	1464	15 US-10-222-772-15 Sequence 1, App1
21	44	44.4	243	17 US-10-739-930-9140 Sequence 1, App1
22	44	44.4	268	15 US-10-434-599-173377 Sequence 173377, Sequence 57369, A
23	44	44.4	432	15 US-10-222-122A-51769 Sequence 3911, AP
24	44	44.4	1042	14 US-10-349-493-23561 Sequence 282496, Sequence 517, App1
25	44	44.4	539	14 US-09-826-502-517 Sequence 440, App1
26	44	44.4	590	14 US-10-225-567A-490 Sequence 440, App1
27	44	44.4	590	14 US-10-322-68A-40 Sequence 440, App1
28	44	44.4	608	13 US-10-029-009-11 Sequence 440, App1
29	44	44.4	626	13 US-10-029-003-23 Sequence 440, App1
30	44	44.4	642	14 US-10-349-493-23561 Sequence 440, App1
31	43	43.4	48	15 US-10-434-593-28296 Sequence 440, App1
32	43	43.4	100	15 US-10-434-599-174021 Sequence 440, App1
33	43	43.4	116	17 US-10-425-115-31282 Sequence 440, App1
34	43	43.4	233	15 US-10-221-622-65 Sequence 440, App1
35	43	43.4	554	16 US-10-437-963-176668 Sequence 440, App1
36	43	43.4	561	14 US-10-034-466-8 Sequence 440, App1
37	43	43.4	16	US-10-437-963-174882 Sequence 440, App1
38	43	43.4	973	14 US-10-156-761-9394 Sequence 440, App1
39	42	42.4	373	15 US-10-424-599-23426 Sequence 440, App1
40	42	42.4	42	15 US-10-424-599-26556 Sequence 440, App1
41	42	42.4	456	9 US-09-764-868-985 Sequence 440, App1
42	42	42.4	691	16 US-10-437-963-176688 Sequence 440, App1
43	42	42.4	151	17 US-10-435-115-364078 Sequence 440, App1
44	42	42.4	190	14 US-10-034-585-7773 Sequence 440, App1
45	42	42.4	269	15 US-10-434-599-14499 Sequence 440, App1
46	42	42.4	373	15 US-10-424-599-23426 Sequence 440, App1
47	42	42.4	373	16 US-10-424-599-131308 Sequence 440, App1
48	42	42.4	456	9 US-09-764-868-985 Sequence 440, App1
49	42	42.4	691	16 US-10-437-963-176688 Sequence 440, App1
50	42	42.4	1148	13 US-10-424-599-14499 Sequence 440, App1
51	41.5	41.9	1055	16 US-10-424-599-23426 Sequence 440, App1
52	41	41.4	98	17 US-10-425-115-31282 Sequence 440, App1
53	41	41.4	233	15 US-10-425-115-367534 Sequence 440, App1
54	41	41.4	122	15 US-10-424-599-276228 Sequence 440, App1
55	41	41.4	156	17 US-10-424-599-266275 Sequence 440, App1
56	41	41.4	242	17 US-10-739-930-9139 Sequence 440, App1
57	41	41.4	244	15 US-10-424-599-234255 Sequence 440, App1
58	41	41.4	253	16 US-10-437-963-169317 Sequence 440, App1
59	41	41.4	255	16 US-10-767-701-40518 Sequence 440, App1
60	41	41.4	268	15 US-10-380-566-534 Sequence 440, App1
61	41	41.4	270	15 US-10-424-599-195447 Sequence 440, App1
62	41	41.4	379	17 US-10-425-115-313892 Sequence 313892, App1
63	41	41.4	389	16 US-10-670-701-47031 Sequence 4031, A
64	41	41.4	392	17 US-10-422-115-314635 Sequence 314635, A
65	41	41.4	395	15 US-10-425-114-56341 Sequence 56341, A
66	41	41.4	487	9 US-09-734-569-176 Sequence 1761, App1
67	41	41.4	542	15 US-10-389-566-641 Sequence 641, App1
68	41	41.4	569	15 US-10-034-585-7191 Sequence 63666, A
69	41	41.4	724	14 US-10-282-122A-63666 Sequence 7191, App1
70	41	41.4	721	16 US-10-408-765M-1897 Sequence 1897, App1
71	41	41.4	73	16 US-10-399-455-17 Sequence 17, App1
72	41	41.4	790	16 US-10-399-455-17 Sequence 17, App1
73	41	41.4	1090	16 US-10-427-963-122130 Sequence 122130, App1
74	41	41.4	1464	9 US-09-945-901-11 Sequence 11, App1
75	41	41.4	1464	9 US-09-945-901-11 Sequence 11, App1
76	41	41.4	1464	10 US-10-007-747-11 Sequence 11, App1
77	41	41.4	1464	14 US-10-038-931-11 Sequence 11, App1
78	41	41.4	1464	14 US-10-243-740-2 Sequence 2, App1
79	41	41.4	1464	17 US-10-473-127-236 Sequence 2, App1
80	41	41.4	1464	17 US-10-473-127-237 Sequence 2, App1
81	41	41.4	1464	17 US-10-473-127-238 Sequence 2, App1
82	41	41.4	1464	17 US-10-473-127-240 Sequence 2, App1
83	41	41.4	1464	17 US-10-473-127-241 Sequence 2, App1
84	41	41.4	1464	17 US-10-473-127-242 Sequence 2, App1
85	41	41.4	1464	17 US-10-473-127-243 Sequence 2, App1
86	41	41.4	1464	17 US-10-473-127-244 Sequence 2, App1

; GENERAL INFORMATION:  
; APPLICANT: McIntire, Jennifer Jones  
; APPLICANT: Umetsu, Dale T.  
; APPLICANT: Dekruyff, Rosemarie  
; APPLICANT: Kuchroo, Vijay  
; APPLICANT: Freeman, Gordon J.  
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: STAN-235  
; CURRENT APPLICATION NUMBER: US/10/188,012  
; CURRENT FILING DATE: 2002-07-01  
; PRIORITY APPLICATION NUMBER: 60/302,344  
; PRIOR FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 17  
; LENGTH: 359  
; TYPE: PRT  
; ORGANISM: H. sapiens  
; FEATURE: VARIANT  
; NAME/KEY: VARIANT  
; LOCATION: (1...360)  
; OTHER INFORMATION: TIM-1 allele 1  
; US-10-188-012-17

QY 1 SSDGLWNNTQLEHS 18  
Db 264 SSDGLWNNTQLEHS 281

RESULT 2

Query Match 100.0%; Score 99; DB 14; Length 359;  
Best Local Similarity 100.0%; Pred. No. 2; 3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-188-012-19

Sequence 19, Application US/10188012  
Publication No. US20030124114A1  
GENERAL INFORMATION:  
APPLICANT: McIntire, Jennifer Jones  
SEQUENCE 167129,  
SEQUENCE 53, APP1  
SEQUENCE 53, APP1  
SEQUENCE 34, APP1  
SEQUENCE 334, APP1  
SEQUENCE 1390, APP1  
SEQUENCE 148, APP1  
SEQUENCE 208, APP1  
SEQUENCE 6237, APP1  
SEQUENCE 41570, APP1  
SEQUENCE 201446, APP1  
SEQUENCE 3, APP1  
SEQUENCE 405, APP1  
SEQUENCE 147295,  
SEQUENCE 363170  
SEQUENCE 350274,  
SEQUENCE 216289,  
SEQUENCE 147, APP1  
SEQUENCE 72, APP1  
SEQUENCE 2191, APP1  
SEQUENCE 72, APP1  
SEQUENCE 339053,  
SEQUENCE 20170,  
SEQUENCE 194265,  
SEQUENCE 253434,  
SEQUENCE 162608,

Query Match 100.0%; Score 99; DB 14; Length 359;  
Best Local Similarity 100.0%; Pred. No. 2; 3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQLEHS 18  
Db 264 SSDGLWNNTQLEHS 281

## ALIGNMENTS

RESULT 1  
US-10-188-012-17  
; Sequence 17, Application US/10188012  
; Publication No. US20030124114A1

RESULT 3

US-10-295-027-302  
; Sequence 302, Application US/10295027  
; Publication No. US20030232350A1  
GENERAL INFORMATION:  
APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glynn, Richard  
APPLICANT: Heveri, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Bob Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and File Reference: 018501-012500US  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR APPLICATION NUMBER: US 60/335,394  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: US 60/332,464  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US 60/334,393  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/340,376  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/347,211  
PRIOR FILING DATE: 2002-01-08  
PRIOR APPLICATION NUMBER: US 60/347,349  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: US 60/355,250  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US 60/356,714  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1386  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 302  
LENGTH: 359  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-295-027-302  
Query Match 100.0%; Score 99; DB 14; Length 359;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 18; Conservative 0; Mismatches 0;  
Indels 0; Gaps 0;  
Qy 1 SSDGLWNNOQTQFLFHS 18  
Db 264 SSDGLWNNOQTQFLFHS 281  
RESULT 5  
US-10-188-012-25  
Sequence 25, Application US/10188012  
Publication No. US20030124114A1  
GENERAL INFORMATION:  
APPLICANT: McIntire, Jennifer Jones  
APPLICANT: Umetsu, Dale T.  
APPLICANT: Dekryff, Rosemarie  
APPLICANT: Kuchroo, Vijay  
APPLICANT: Freeman, Gordon J.  
TITLE OF INVENTION: T Cell Regulatory Genes and Methods of File Reference: STAN-235  
CURRENT FILING DATE: 2002-07-01  
PRIOR APPLICATION NUMBER: 60/302,344  
PRIOR FILING DATE: 2001-06-29  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 364  
TYPE: PRT  
ORGANISM: H. sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)..(364)  
OTHER INFORMATION: TIM-1 allele 5  
US-10-188-012-25  
Query Match 100.0%; Score 99; DB 14; Length 364;  
Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
Matches 18; Conservative 0; Mismatches 0;  
Indels 0; Gaps 0;  
Qy 1 SSDGLWNNOQTQFLFHS 18  
Db 269 SSDGLWNNOQTQFLFHS 286  
RESULT 6  
US-10-188-012-27  
Sequence 27, Application US/10188012  
Publication No. US20030124114A1  
GENERAL INFORMATION:  
APPLICANT: McIntire, Jennifer Jones  
APPLICANT: Umetsu, Dale T.  
APPLICANT: Dekryff, Rosemarie  
APPLICANT: Kuchroo, Vijay  
APPLICANT: Freeman, Gordon J.

; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: STAN-235  
; CURRENT APPLICATION NUMBER: US/10/188,012  
; CURRENT FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/302,344  
; PRIOR FILING DATE: 2001-06-29  
; SEQ ID NO: 36  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 27  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)..(364)  
; OTHER INFORMATION: TIM-1, allele 6  
; US-10-188-012-27

RESULT 7  
; Sequence Match 100.0%; Score 99; DB 14; Length 364;  
; Best Local Similarity 100.0%; Pred. No. 2.4e-07; Mismatches 0; Indels 0; Gaps 0;  
; Matches 18; Conservative 0; Name/Key: VARIANT  
; QY 1 SSDGGLWNNTQOLFLEHS 18  
; Db 269 SSDGGLWNNTQOLFLEHS 286

US-10-188-012-21  
; Sequence 21, Application US/10188012  
; GENERAL INFORMATION:  
; APPLICANT: McIntire, Jennifer Jones  
; APPLICANT: Umetsu, Dale T.  
; APPLICANT: Dekruyff, Rosemarie  
; APPLICANT: Kuchroo, Vijay  
; APPLICANT: Freeman, Gordon J.  
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: STAN-235  
; CURRENT APPLICATION NUMBER: US/10/188,012  
; CURRENT FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/302,344  
; PRIOR FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 21  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)..(365)  
; OTHER INFORMATION: TIM-1, allele 3  
; US-10-188-012-21

RESULT 9  
; Sequence Match 94.9%; Score 94; DB 14; Length 359;  
; Best Local Similarity 94.4%; Pred. No. 1.5e-06; Mismatches 0; Indels 0; Gaps 0;  
; Matches 17; Conservative 1; Name/Key: VARIANT  
; QY 1 SSDGGLWNNTQOLFLEHS 18  
; Db 264 SSDGGLWNNTQOLFLEHS 281

US-09-991-258-13  
; Sequence 13, Application US/09991258  
; Patent No. US20020141975A1  
; GENERAL INFORMATION:  
; APPLICANT: Olmsted, Robert  
; APPLICANT: Keith, Paula  
; APPLICANT: Driga, Sergey  
; APPLICANT: Cailey, Ian  
; APPLICANT: Maughan, Maureen  
; APPLICANT: Johnston, Robert  
; APPLICANT: Davis, Nancy  
; APPLICANT: Swanstrom, Ronald  
; TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE IN  
; TITLE OF INVENTION: VACCINES  
; FILE REFERENCE: 01113.0001U3  
; CURRENT APPLICATION NUMBER: US/09/991,258  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 09/902,537  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/216,995  
; PRIOR FILING DATE: 2000-07-07  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 13  
; LENGTH: 981  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1= US-09-991-258-13

Query Match 100.0%; Score 99; DB 14; Length 365;  
; Best Local Similarity 100.0%; Pred. No. 2.4e-07; Mismatches 0; Indels 0; Gaps 0;  
; Matches 18; Conservative 0; Name/Key: VARIANT  
; QY 1 SSDGGLWNNTQOLFLEHS 18  
; Db 270 SSDGGLWNNTQOLFLEHS 287

RESULT 8  
; Sequence 23, Application US/10188012  
; Publication No. US20030124114A1  
; GENERAL INFORMATION:  
; APPLICANT: McIntire, Jennifer Jones  
; APPLICANT: Umetsu, Dale T.

RESULT 10  
US-10-424-599-175126  
; Sequence 175126, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: JAB-1667  
; CURRENT APPLICATION NUMBER: US/10/451,467A  
; PRIORITY NUMBER: EP 01870003.9  
; PRIORITY NUMBER: EP 01870002.1  
; PRIORITY FILING DATE: 2001-01-09  
; PRIORITY FILING DATE: 2000-12-22  
; PRIORITY FILING DATE: 2001-01-04  
; PRIORITY FILING DATE: 2001-01-09  
; NUMBER OF SEQ ID NOS: 732  
; SEQ ID NO: 56  
; LENGTH: 508  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_129157C.1.pep  
US-10-424-599-175126  
Query Match 47.5%; Score 47; DB 15; Length 102;  
Best Local Similarity 60.0%; Pred. No. 11; Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 1 SDGJLWNNTTQLFL 15  
Db 79 STQGDWINNTHLU 93  
RESULT 11  
US-10-369-493-1469  
; Sequence 1469, Application US/10369493  
; Publication No. US2003010235675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinklin, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10 (52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/350,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO: 1469  
; LENGTH: 508  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-369-493-1469  
Query Match 46.5%; Score 46; DB 14; Length 508;  
Best Local Similarity 63.6%; Pred. No. 86; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 6 WANNQTLFL 16  
Db 160 WNNNNSMFL 170  
RESULT 13  
US-10-389-566-1218  
; Sequence 1218, Application US/10389566  
; Publication No. US200400525202A1  
; GENERAL INFORMATION:  
; APPLICANT: Monstanto Technology, LLC  
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants  
; FILE REFERENCE: 38-77 (52000)D  
; CURRENT APPLICATION NUMBER: US/10/389,566  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/365,301  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/391,786  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/392,018  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 2459  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 1218  
; LENGTH: 545  
; TYPE: PRT  
; ORGANISM: Solanum tuberosum  
US-10-389-566-1218  
Query Match 45.5%; Score 46; DB 15; Length 545;  
Best Local Similarity 57.1%; Pred. No. 92; Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 3 DGLWNNTTQLFL 16  
Db 324 DGTWNSEYGGFL 337  
RESULT 14  
US-10-437-963-163657  
; Sequence 163657, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
RESULT 12  
US-10-451-467A-56  
; Sequence 56, Application US/10451467A  
; Publication No. US20040161840A1  
; GENERAL INFORMATION:  
; APPLICANT: CONTRERAS, ROLAND HENRI  
; APPLICANT: EBERHARD, INES  
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS

APPLICANT: Boukharov, Andrey A.  
 APPLICANT: Barbazuk, Brad  
 APPLICANT: Li, Ping  
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title Reference: 38-21(53221)B  
 CURRENT APPLICATION NUMBER: US10/437,963  
 CURRENT FILING DATE: 2003-05-14  
 NUMBER OF SEQ ID NOS: 204966  
 SEQ ID NO: 163657  
 LENGTH: 384  
 TYPE: PRT  
 ORGANISM: Oryza sativa  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT4530\_62632C.1.pep  
 US-10-437-963-163657

Query Match 46.0%; Score 45.5; DB 16; Length 384;  
 Best Local Similarity 61.1%; Pred. No. 77;  
 Matches 11; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 1 SDG---LWNNTQFL 15  
 Db 168 SDDGSVKLWNNTQFL 185

RESULT 15  
 US-10-437-963-163658  
 Sequence 163658, Application US/10437963  
 Publication No. US20040123343A1

GENERAL INFORMATION:  
 APPLICANT: Li, Rosa, Thomas J.  
 APPLICANT: Kovacic, David K.  
 APPLICANT: Zhou, Yinhua  
 APPLICANT: Cao, Yongwei  
 APPLICANT: Wu, Wei  
 APPLICANT: Boukharov, Andrey A.  
 APPLICANT: Barbazuk, Brad  
 APPLICANT: Li, Ping  
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title Reference: 38-21(53221)B  
 CURRENT APPLICATION NUMBER: US10/437,963  
 CURRENT FILING DATE: 2003-05-14  
 NUMBER OF SEQ ID NOS: 204966  
 SEQ ID NO: 163658  
 LENGTH: 770  
 TYPE: PRT  
 ORGANISM: Oryza sativa  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (1)..(770)  
 OTHER INFORMATION: unsure at all xaa locations  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT4530\_62633C.1.pep  
 US-10-437-963-163658

Query Match 46.0%; Score 45.5; DB 16; Length 770;  
 Best Local Similarity 61.1%; Pred. No. 1.6e-02;  
 Matches 11; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 1 SDG---LWNNTQFL 15  
 Db 554 SDDGSVKLWNNTQFL 571

RESULT 16  
 US-10-156-761-9511  
 Sequence 9511, Application US/10156761  
 Publication No. US20030119018A1  
 GENERAL INFORMATION:  
 APPLICANT: OMURA, SATOSHI  
 APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN  
 APPLICANT: HORIKAWA, HIROSHI  
 APPLICANT: SHIBA, TADAYOSHI  
 APPLICANT: SAKAKI, YOSHITAKE  
 APPLICANT: HATTORI, MASAHIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 24-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: JP 2001-272697  
 PRIOR FILING DATE: 2001-08-02  
 NUMBER OF SEQ ID NOS: 15109  
 SEQ ID NO: 9511  
 LENGTH: 273  
 TYPE: PRT  
 ORGANISM: Streptomyces avermitilis  
 US-10-156-761-9511

Query Match 45.5%; Score 45; DB 14; Length 273;  
 Best Local Similarity 56.2%; Pred. No. 64;  
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 SDGWNNTQFLF 17  
 Db 126 SGGEWGRGLFQFLFH 141

RESULT 17  
 US-10-282-122A-48522  
 Sequence 48522, Application US/10282122A  
 Publication No. US20040029129A1

GENERAL INFORMATION:  
 APPLICANT: Wang, Liangbu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari  
 APPLICANT: Zveckind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELTRIA-034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20  
 PRIOR APPLICATION NUMBER: 60191,078  
 PRIOR FILING DATE: 2000-03-221  
 PRIOR APPLICATION NUMBER: 601206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 601207,727  
 PRIOR FILING DATE: 2000-05-25  
 PRIOR APPLICATION NUMBER: 601230,335  
 PRIOR FILING DATE: 2000-09-05  
 PRIOR APPLICATION NUMBER: 601230,347  
 PRIOR FILING DATE: 2000-09-09  
 PRIOR APPLICATION NUMBER: 601242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 601253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 601257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 601267,636  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 601269,308  
 PRIOR FILING DATE: 2001-02-16  
 Remaining prior application data removed - See file wrapper or PALM  
 NUMBER OF SEQ ID NOS: 78614  
 SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 48522  
; LENGTH: 687  
; TYPE: PRT  
; ORGANISM: *Bacteroides fragilis*  
; US-10-582-12A-45522

Query Match 45.5%; Score 45; DB 15; Length 687;  
Best local Similarity 54.5%; Pred. No. 1.7e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 5; Mismatches 0; SEQ ID NO: 1; LENGTH: 1464  
TYPE: PRT  
ORGANISM: *Bacteroides fragilis*

RESULT 18  
US-09-934-070-15  
Sequence 15, Application US/09934070  
Publication No. US20030092004A1  
GENERAL INFORMATION:  
APPLICANT: Lipton, Stuart A.  
APPLICANT: Zhang, Dongxian  
APPLICANT: Chatterton, Jon E.  
APPLICANT: Awobuluyi, Marc A.  
APPLICANT: Sevarino, Kevin A.  
TITLE OF INVENTION: EXCITATORY GLYCINE RECEPTORS AND METHODS  
FILE REFERENCE: P-LJ 4900  
CURRENT APPLICATION NUMBER: US/09/934,070  
CURRENT FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 1464  
TYPE: PRT  
ORGANISM: *Rattus sp.*

US-09-934-070-15

Query Match 45.5%; Score 45; DB 10; Length 1464;  
Best Local Similarity 47.1%; Pred. No. 3.8e+02; Indels 0; Gaps 0;  
Matches 8; Conservative 5; Mismatches 4; SEQ ID NO: 1; LENGTH: 1464  
TYPE: PRT  
ORGANISM: *Rattus sp.*

RESULT 19  
US-09-932-011-1  
Sequence 1, Application US/09922011  
Publication No. US2003009331A1  
GENERAL INFORMATION:  
APPLICANT: CIS Biotech, Inc.  
APPLICANT: Dambinova, Svetlana  
TITLE OF INVENTION: Rapid multiple panel of biomarkers in laboratory blood tests for TITLE OF INVENTION: TIA stroke  
FILE REFERENCE: 08B05.103001  
CURRENT APPLICATION NUMBER: US/09/932,011  
CURRENT FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1464  
TYPE: PRT  
ORGANISM: *homo sapiens*

US-09-922-011-1

Query Match 45.5%; Score 45; DB 10; Length 1464;  
Best Local Similarity 47.1%; Pred. No. 3.8e+02; Indels 0; Gaps 0;  
Matches 8; Conservative 5; Mismatches 4; SEQ ID NO: 1; LENGTH: 1464  
TYPE: PRT  
ORGANISM: *homo sapiens*

RESULT 20  
US-10-222-772-15  
Sequence 15, Application US/10222772  
Publication No. US20040033500A1  
GENERAL INFORMATION:  
APPLICANT: Lipton, Stuart A.  
APPLICANT: Zhang, Dongxian  
APPLICANT: Chatterton, Jon E.  
APPLICANT: Awobuluyi, Marc A.  
APPLICANT: Sevarino, Kevin A.  
TITLE OF INVENTION: EXCITATORY GLYCINE RECEPTORS AND METHODS  
FILE REFERENCE: P-LJ 5338  
CURRENT APPLICATION NUMBER: US/10/222,772  
PRIOR APPLICATION NUMBER: US 09/934,070  
PRIORITY FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 1464  
TYPE: PRT  
ORGANISM: *Rattus sp.*

US-10-222-772-15

Query Match 45.5%; Score 45; DB 15; Length 1464;  
Best Local Similarity 47.1%; Pred. No. 3.8e+02; Indels 0; Gaps 0;  
Matches 8; Conservative 5; Mismatches 4; SEQ ID NO: 1; LENGTH: 1464  
TYPE: PRT  
ORGANISM: *Rattus sp.*

RESULT 21  
US-10-739-930-9140  
Sequence 9340, Application US/10739930  
Publication No. US20040216190A1  
GENERAL INFORMATION:  
APPLICANT: Kovacic, David K.  
TITLE OF INVENTION: PLANTS AND USBS THEREOF FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-21(5337)B  
CURRENT APPLICATION NUMBER: US/10/739,930  
CURRENT FILING DATE: 2003-12-18  
NUMBER OF SEQ ID NOS: 11088  
SEQ ID NO 9140  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE: OTHER INFORMATION: Clone ID: GLYMA-23APR03-C4363\_4.p  
US-10-739-930-9140

Query Match 44.4%; Score 44; DB 17; Length 243;  
Best Local Similarity 52.9%; Pred. No. 82; Indels 2; Gaps 1;  
Matches 9; Conservative 1; Mismatches 5; SEQ ID NO: 2; LENGTH: 1464  
TYPE: PRT  
ORGANISM: Glycine max

RESULT 22  
US-10-424-599-173377  
Sequence 173377, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J  
APPLICANT: Kovalic, David K  
APPLICANT: Zhou Yiniua  
APPLICANT: Cao Yongwei

RESULT 23  
US-10-282-122A-57369  
; Sequence 57369, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zykkind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trowick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsbyth, R.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA-034A  
; CURRENT APPLICATION NUMBER: US11/01282,122A  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-05-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-03-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 7614  
; SOFTWARE: PatentIn Version 3.1  
; SEQ ID NO: 57369  
; LENGTH: 432  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
; US-10-282-122A-57369

RESULT 24  
US-10-369-493-3911  
; Sequence 3911, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO: 3911  
; LENGTH: 539  
; TYPE: PRT  
; ORGANISM: Neurospora crassa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(539)  
; OTHER INFORMATION: unsure at all Xaa locations  
; US-10-369-493-3911

RESULT 25  
US-09-826-509-517  
; Sequence 509, Application US/09826509  
; Publication No. US20030204073A1  
; GENERAL INFORMATION:  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: NO. US20030204073A1-Endogenous, Constitutively Activated Known G  
; TITLE OF INVENTION: Protein-Coupled Receptors  
; FILE REFERENCE: ARBN-207  
; CURRENT APPLICATION NUMBER: US/09/826,509  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/195,747  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 589  
; SOFTWARE: PatentIn Version 2.1  
; SEQ ID NO: 517  
; LENGTH: 590  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-826-509-517

Query Match 44.4%; Score 44; DB 10; Length 590;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: US 60/399,783  
 PRIOR FILING DATE: 2002-07-31  
 PRIOR APPLICATION NUMBER: US 60/403,221  
 PRIOR FILING DATE: 2002-08-13  
 Remaining Prior Application data removed - See File Wrapper or PALM.

RESULT 26  
 US-10-225-567A-440  
 ; Sequence 440, Application US/10225567A  
 ; Publication No. US20030113798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lifespan Biosciences  
 ; APPLICANT: Brown, Joseph P.  
 ; APPLICANT: Burner, Glenna C.  
 ; APPLICANT: Roush, Christine L.  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
 ; CURRENT APPLICATION NUMBER: US/10/225,567A  
 ; CURRENT FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 60/257,144  
 ; PRIOR FILING DATE: 2000-12-19  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 440  
 ; LENGTH: 590  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-225-567A-440

Query Match 44.4%; Score 44; DB 14; Length 590;  
 Best Local Similarity 50.0%; Pred. No. 2.1e+02; Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQFLFHS 18  
 Db 332 SSSDSWNNDAAASLENS 349

RESULT 27  
 US-10-352-684A-40  
 ; Sequence 40, Application US/10352684A  
 ; Publication No. US20030215452A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals Inc.  
 ; APPLICANT: Carroll, Joseph M.  
 ; APPLICANT: Healy, Aileen  
 ; APPLICANT: Welch, Nadine S.  
 ; APPLICANT: Kelly, Louise M.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906, 15513, 17822, 30, 5677, 194, 14393, 2059, 7365, 12212, 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES  
 ; FILE REFERENCE: MPI02-0191RN0NM  
 ; CURRENT APPLICATION NUMBER: US/10/352,684A  
 ; CURRENT FILING DATE: 2003-01-28  
 ; PRIOR APPLICATION NUMBER: US 60/354,333  
 ; PRIOR FILING DATE: 2002-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/360,258  
 ; PRIOR FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/364,476  
 ; PRIOR FILING DATE: 2002-03-15  
 ; PRIOR APPLICATION NUMBER: US 60/375,626  
 ; PRIOR FILING DATE: 2002-04-26  
 ; PRIOR APPLICATION NUMBER: US 60/386,494  
 ; PRIOR FILING DATE: 2002-06-06  
 ; PRIOR APPLICATION NUMBER: US 60/390,965  
 ; PRIOR FILING DATE: 2002-06-24  
 ; PRIOR APPLICATION NUMBER: US 60/392,480  
 ; PRIOR FILING DATE: 2002-06-28  
 ; PRIOR APPLICATION NUMBER: US 60/394,128  
 ; PRIOR FILING DATE: 2002-07-03

Query Match 44.4%; Score 44; DB 14; Length 590;  
 Best Local Similarity 50.0%; Pred. No. 2.1e+02; Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQFLFHS 18  
 Db 332 SSSDSWNNDAAASLENS 349

RESULT 28  
 US-10-029-009-11  
 ; Sequence 11, Application US/10029009  
 ; Publication No. US20020164617A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Felsch, Jason S.  
 ; APPLICANT: Annis, David Allen  
 ; APPLICANT: Kalghatgi, Krishna  
 ; APPLICANT: Nash, Haw M.  
 ; TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins  
 ; CURRENT APPLICATION NUMBER: US/10/029,009  
 ; CURRENT FILING DATE: 2002-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/258,970  
 ; PRIOR FILING DATE: 2000-12-29  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 11  
 ; LENGTH: 608  
 ; TYPE: PRT  
 ; ORGANISM: Rat  
 ; US-10-029-009-11

Query Match 44.4%; Score 44; DB 13; Length 608;  
 Best Local Similarity 50.0%; Pred. No. 2.0e+02; Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQFLFHS 18  
 Db 331 SSSDSWNNDAAASLENS 348

RESULT 29  
 US-10-029-009-23  
 ; Sequence 23, Application US/10029009  
 ; Publication No. US20020164617A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Felsch, Jason S.  
 ; APPLICANT: Annis, David Allen  
 ; APPLICANT: Kalghatgi, Krishna  
 ; APPLICANT: Nash, Haw M.  
 ; TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins  
 ; FILE REFERENCE: 11025.173 US2  
 ; CURRENT APPLICATION NUMBER: US/10/029,009  
 ; CURRENT FILING DATE: 2002-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/258,970  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 23  
 ; LENGTH: 626

```

; TYPE: PRT
; ORGANISM: Rat
US-10-029-009-23

Query Match
Best Local Similarity 44.4%; Score 44; DB 13; Length 626;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
Qy 1 SDGLIWNNOTQLEHS 18
Db 347 SSSDWNNDAAASLENS 364

RESULT 30
US-10-369-493-23561
; Sequence 23561, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkl, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10/52052B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23561
; LENGTH: 1042
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-369-493-23561

Query Match
Best Local Similarity 44.4%; Score 44; DB 14; Length 1042;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 3 DGLIMNNQNOTQLEH 17
Db 788 EGLWQPNHQIMQEH 802

RESULT 31
US-10-424-599-282496
; Sequence 282496, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21/53233B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 282496
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_97115C.1.pep
US-10-424-599-282496

Query Match
Best Local Similarity 43.4%; Score 43; DB 15; Length 48;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 5 LWNNOTQLEHS 18
Db 22 LMNSNHTEGLIKHN 35

RESULT 32
US-10-424-599-174021
; Sequence 174021, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21/53233B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174021
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(100)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_128159C.1.pep
US-10-424-599-174021

Query Match
Best Local Similarity 43.4%; Score 43; DB 15; Length 100;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 5 LWNNOTQLEH 16
Db 84 LMNNHQIEFFVD 95

RESULT 33
US-10-425-115-312882
; Sequence 312882, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21/53222B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 312882
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_48408C.1.pep
US-10-425-115-312882

Query Match
Best Local Similarity 43.4%; Score 43; DB 17; Length 116;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 5 LMNNQNOTQLEHS 18
Db 22 LMNSNHTEGLIKHN 35

```

RESULT 34  
US-10-221-625-65  
; Sequence 55, Application US/10221625  
; Publication No. US20040033942A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: YUE, Henry  
; APPLICANT: LAL, Preeti  
; APPLICANT: LU, Duyng Aina M.  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: MATRUR, Preete  
; APPLICANT: SHAH, Purvi  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: REDDI, Roopa  
TITLE OF INVENTION: TRANSCRIPTION FACTORS  
FILE REFERENCE: PP-0761 PCT  
CURRENT APPLICATION NUMBER: US/10/221,625  
CURRENT FILING DATE: 2001-03-13  
NUMBER OF SEQ ID NOS: 214  
SOFTWARE: PERL\_Program  
SEQ ID NO: 65  
LENGTH: 233  
TYPE: PRT  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No. US20040033942A1 2646274CD1  
US-10-221-625-65

Query Match 43.4%; Score 43; DB 15; Length 233;  
Best Local Similarity 47.1%; Pred. No. 1.1e+02;  
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 SSDGLWNNTQOLEH 17  
Db 75 STEGLFNMGFAEFLH 91

RESULT 35  
US-10-437-963-176868  
; Sequence 176868, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 176868  
LENGTH: 554  
TYPE: PRT  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_74577C.1.pep  
US-10-437-963-176868

Query Match 43.4%; Score 43; DB 16; Length 554;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

RESULT 36  
US-10-094-466-8  
; Sequence 8, Application US/10094466  
; Publication No. US20030203363A1  
; GENERAL INFORMATION:  
; APPLICANT: SPYCE et al.  
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM  
TITLE OF INVENTION: AND METHODS OF USING  
FILE REFERENCE: 21402-290D  
CURRENT APPLICATION NUMBER: US/10/094,466  
CURRENT FILING DATE: 2002-03-07  
PRIORITY APPLICATION NUMBER: 60/274,281  
PRIORITY FILING DATE: 2001-03-08  
PRIORITY APPLICATION NUMBER: 60/288,148  
PRIORITY FILING DATE: 2001-05-02  
PRIORITY APPLICATION NUMBER: 60/274,849  
PRIORITY FILING DATE: 2001-03-09  
PRIORITY APPLICATION NUMBER: 60/275,235  
PRIORITY FILING DATE: 2001-03-12  
PRIORITY APPLICATION NUMBER: 60/338,375  
PRIORITY FILING DATE: 2001-12-4  
PRIORITY APPLICATION NUMBER: 60/275,579  
PRIORITY FILING DATE: 2001-03-13  
PRIORITY APPLICATION NUMBER: 60/335,302  
PRIORITY FILING DATE: 2001-10-31  
PRIORITY APPLICATION NUMBER: 60/275,601  
PRIORITY FILING DATE: 2001-03-13  
PRIORITY APPLICATION NUMBER: 60/276,000  
PRIORITY FILING DATE: 2001-03-14  
PRIORITY APPLICATION NUMBER: 60/277,338  
PRIORITY FILING DATE: 2001-03-20  
PRIORITY APPLICATION data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: Patin 2.1  
SEQ ID NO: 8  
LENGTH: 561  
TYPE: PRT  
FEATURE:  
NAME/KEY: Homo sapiens  
OTHER INFORMATION: Incyte ID No. US20040123343A1  
US-10-094-466-8

Query Match 43.4%; Score 43; DB 14; Length 561;  
Best Local Similarity 47.1%; Pred. No. 2.8e+02;  
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 SSDGLWNNTQOLEH 17  
Db 279 STEGLFNMGFAEFLH 295

RESULT 37  
US-10-437-963-174682  
; Sequence 174682, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14  
 NUMBER OF SEQ ID NOS: 204966  
 SEQ ID NO: 174682  
 LENGTH: 684  
 TYPE: PRT  
 ORGANISM: *Oryza sativa*  
 OTHER INFORMATION: Clone ID: PAT\_MRT4530\_725C.1.pep  
 US-10-437-963-174682

Query Match 43.4%; Score 43; DB 16; Length 684;  
 Best Local Similarity 63.6%; Pred. No. 3.5e-02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LWNNNQTOFL 15  
 Db 431 LWSNNKKELFL 441

RESULT 38  
 US-10-158-761-9394  
 Sequence 9394, Application US/10156761  
 Publication No. US20030119018A1  
 GENERAL INFORMATION:  
 APPLICANT: OMURA, SATOSHI  
 APPLICANT: IKEDA, HARUO  
 APPLICANT: ISHIKAWA, JUN  
 APPLICANT: HORIKAWA, HIROSHI  
 APPLICANT: SHIBA, TADAYOSHI  
 APPLICANT: SAKAKI, YOSHITUKI  
 APPLICANT: HATTORI, MASAMIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: JP 2001-272697  
 PRIOR FILING DATE: 2001-06-02  
 NUMBER OF SEQ ID NOS: 15109  
 SEQ ID NO: 9394  
 LENGTH: 973  
 TYPE: PRT  
 ORGANISM: *Streptomyces avermitilis*  
 US-10-156-761-9394

Query Match 43.4%; Score 43; DB 14; Length 973;  
 Best Local Similarity 63.6%; Pred. No. 5.1e-02; Mismatches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 DGLWMNNQTOI 13  
 Db 872 DGMMWNNYQDSL 882

RESULT 39  
 US-10-424-599-265756  
 Sequence 265756, Application US/10424599  
 Publication No. US20040031072A1  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa, Thomas J  
 APPLICANT: Kovacic, David K.  
 APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 FILE REFERENCE: 3-21(5222)B  
 CURRENT APPLICATION NUMBER: US/10/425,115  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 367358  
 SEQ ID NO: 367358  
 LENGTH: 50  
 TYPE: PRT  
 ORGANISM: *Zea mays*  
 FEATURE:  
 OTHER INFORMATION: Clone ID: MRT4577\_98200C.1.pep  
 US-10-425-115-367358

Query Match 42.4%; Score 42; DB 17; Length 50;  
 Best Local Similarity 42.9%; Pred. No. 32; Mismatches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 5 LWNNNQTOFLEHS 18  
 Db 9 VWSNHRVRFLOHS 22

Search completed: December 30, 2004, 16:25:32  
 Job time : 147 secs

FILE REFERENCE: 38-21(5322)B  
 CURRENT APPLICATION NUMBER: US/10/424,599  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 285684  
 SEQ ID NO: 265756  
 LENGTH: 42  
 TYPE: PRT

Copyright (c) 1993 - 2004 CompuGen Ltd.

GenCore version 5.1.5

Run on: December 30, 2004, 16:14:08 ; Search time 152 Seconds  
 (without alignment)  
 42.481 Million cell updates/sec

X	99	29	29.3	17	4	BAU72451	PN
X	100	29	29.3	19	4	ABR24664	XX
C	101	29	29.3	20	6	ABR2459	PD
C	102	29	29.3	20	8	Group A	12-DEC-2002.
C	103	29	29.3	20	8	Adh7233	XX
X	104	29	29.3	20	8	Adh7234	XX
X	105	28.5	28.8	15	8	Epstein B	31-MAY-2002; 2002WO-US017402.
X	106	28	28.3	8	8	Adm29217	XX
X	107	28	28.3	8	2	Hepatitis	XX
X	108	28	28.3	8	2	Adm2217	PR 01-JUN-2001; 2001US-0295449P.
X	109	28	28.3	8	3	Adp26565	PR 04-JUN-2001; 2001US-0295907P.
X	110	28	28.3	8	5	Plasmodiu	XX
X	111	28	28.3	8	5	Raw15980	XX
X	112	28	28.3	8	7	Intelexuk	XX
X	113	28	28.3	8	8	Raw15819	XX
X	114	28	28.3	8	8	Random pe	XX
X	115	28	28.3	9	2	Aaws8619	PA (BIOT ) BIOGEN INC.
X	116	28	28.3	9	6	Aaws8094	PA (GEHO ) GEN HOSPITAL CORP.
X	117	28	28.3	9	6	Aay09742	XX
X	118	28	28.3	9	6	Aab17545	XX
X	119	28	28.3	9	6	Abt73147	PI
X	120	28	28.3	9	6	VIP-mimet	Bailly V, Bonventre J;
X	121	28	28.3	10	6	ADJ73301	XX
X	122	28	28.3	10	6	Vasoactive	DR WPI; 2003-156845/15.
X	123	28	28.3	10	6	ADJ5235	XX
X	124	28	28.3	10	6	ABR12361	XX
X	125	28	28.3	10	6	ABR11863	PS
X	126	28	28.3	10	6	ABR11854	PT
X	127	28	28.3	12	2	ABR12318	PT
X	128	28	28.3	12	2	Human can	PT
X	129	28	28.3	12	2	ABR12482	XX
X	130	28	28.3	12	2	ABR12695	XX
X	131	28	28.3	12	2	ABR11909	XX
X	132	28	28.3	12	2	AAW58090	XX
X	133	28	28.3	12	4	AAW5091	Sequence 18 AA;
X	134	28	28.3	13	3	Peptide S	Query Match 100.0%; Score 99; DB 6; Length 18;
X	135	28	28.3	13	5	Aab50187	Best Local Similarity 100.0%; Pred. No. 4; Te-08;
X	136	28	28.3	13	5	Aay94566	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
X	137	28	28.3	13	6	AAE72727	OY 1 SSDGELWNNTQTLPLHHS 18
X	138	28	28.3	13	7	ADJ79122	Db 1 SSDGELWNNTQTLPLHHS 18
X	139	28	28.3	14	2	ADG65480	XX
X	140	28	28.3	14	3	ADG65580	RESULT 2
X	141	28	28.3	14	4	Aar69361	AAE33009 Human int
X	142	28	28.3	14	5	Aay94563	Adg65580 Human IL-
X	143	28	28.3	14	5	AAE33009	Adg65580 Human IL-
X	144	28	28.3	14	5	ABJ00739	Aae33009 Human int
X	145	28	28.3	14	5	ABJ00775	Adg65580 Human IL-
X	146	28	28.3	14	5	ABJ00765	Adg65580 Human IL-
X	147	28	28.3	14	5	ABG33636	Adg65580 Human IL-
X	148	28	28.3	14	5	ABG33626	Adg65580 Human IL-
X	149	28	28.3	14	5	ABG33600	Adg65580 Human IL-
X	150	28	28.3	14	6	ADA0332	Ado0332 Angiotensin
X	14	28.3	14	6	6	ABR56702	Abt56702 Angiotensin
<b>ALIGNMENTS</b>							
X	1	RESULT 1	XX	XX	XX	Cytostatic; gene therapy; antibody; antigen; antigen-binding; renal disease; injury; renal cancer; binding epitope.	KW
X	2	AAO26687	XX	XX	XX	proteolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer.	KW
X	3	AAO26687	XX	XX	XX	Homo sapiens.	KW
X	4	AAO26687;	XX	XX	XX	Monoclonal antibody binding epitope, SEQ ID No 1.	DE
X	5	20-MAR-2003	XX	XX	XX	(first entry)	20-MAR-2003
X	6	Human KIM-1 mucin domain related peptide, SEQ ID No 15.	XX	XX	XX	Cytostatic; gene therapy; antibody; antigen; antigen-binding; renal disease; injury; renal cancer.	OS
X	7	Cytostatic; gene therapy; antibody; antigen; antigen-binding; proteolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer.	XX	XX	XX	Synthetic.	OS
X	8	Bailey V, Bonventre J;	XX	XX	XX	12-DEC-2002.	PI
X	9	20-MAR-2003 (first entry)	XX	XX	XX	31-MAY-2002; 2002WO-US017402.	XX
X	10	Human KIM-1 mucin domain related peptide, SEQ ID No 15.	XX	XX	XX	01-JUN-2001; 2001US-0295449P.	XX
X	11	Cytostatic; gene therapy; antibody; antigen; antigen-binding; proteolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer.	XX	XX	XX	04-JUN-2001; 2001US-0295907P.	XX
X	12	Bailey V, Bonventre J;	XX	XX	XX	(BIOJ ) BIOGEN INC.	PA
X	13	20-MAR-2003 (first entry)	XX	XX	XX	(GEHO ) GEN HOSPITAL CORP.	PA
X	14	Human KIM-1 mucin domain related peptide, SEQ ID No 15.	XX	XX	XX	Bailey V, Bonventre J;	PI
X	15	Cytostatic; gene therapy; antibody; antigen; antigen-binding; proteolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer.	XX	XX	XX	WO20029920-A1.	XX

DR WPI; 2003-156845/15.

PT New antibody, antibody derivative or antigen-binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 polypeptide, useful for treating or preventing renal disease or injury, e.g. renal cancer.

PT e.g. renal cancer.

PS Claim 4; Page 25; 42pp; English.

XX

CC The invention relates to a novel antibody, antibody derivative or antigen-binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells. The antibody, antibody derivative or antigen-binding polypeptide is useful for treating or preventing renal disease or injury, e.g. renal cancer. The antibody is also useful for inhibiting shedding of the KIM-1 polypeptide. This sequence represents a binding epitope of the invention

XX

SQ Sequence 18 AA;

Query Match	100.0%	Score	99	DB	6	Length	18
Best Local Similarity	100.0%	Pred.	No.	4.7e-08			
Matches	18	Mismatches	0	Indels	0	Gaps	0

Oy 1 SSDGLWNNNOTQLEHS 18

Db 1 SSDGLWNNNOTQLEHS 18

RESULT 3

ID	AA026686	Standard; peptide; 18 AA.					
XX							
AC	AA026686;						
XX							
DT	20-MAR-2003 (first entry)						
XX							
DE	Human KIM-1 mucin domain related peptide, SEQ ID No 14.						
XX							
DE	Cyostatic; gene therapy; antibody; antigen; antigen-binding; proteolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer.						
XX							
OS	Synthetic.						
XX							
PN	WO20029920-A1.						
XX							
PD	12-DEC-2002.						
XX							
PF	31-MAY-2003 (first entry)						
XX							
PR	01-JUN-2001; 2001US-0295449P.						
PR	04-JUN-2001; 2001US-0295907P.						
XX							
PA	(BIOJ ) BIOPEN INC.						
PA	(GEHO ) GEN HOSPITAL CORP.						
PT	Bailly V, Bonventre J;						
XX							
DR	WPI; 2003-156845/15.						
XX							
PT	New antibody, antibody derivative or antigen-binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 polypeptide, useful for treating or preventing renal disease or injury, e.g. renal cancer.						
XX							
PR	01-JUN-2001; 2001US-0295449P.						
PR	04-JUN-2001; 2001US-0295907P.						
XX							
PA	(BIOJ ) BIOPEN INC.						
PA	(GEHO ) GEN HOSPITAL CORP.						
XX							
PT	Bailly V, Bonventre J;						
XX							
DR	WPI; 2003-156845/15.						
XX							
PT	New antibody, antibody derivative or antigen-binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 polypeptide, useful for treating or preventing renal disease or injury, e.g. renal cancer.						
XX							
PS	Disclosure; Fig 1A; 42pp; English.						
XX							
CC	The invention relates to a novel antibody, antibody derivative or antigen-binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells. The antibody, antibody derivative or antigen-binding polypeptide is useful for treating or preventing renal disease or injury, e.g. renal cancer. The antibody is also useful for inhibiting shedding of the KIM-1 polypeptide. This sequence represents a human KIM-1 mucin domain related peptide of the invention						
XX							
SQ	Sequence 18 AA;						
Query Match	100.0%	Score	99	DB	6	Length	18
Best Local Similarity	100.0%	Pred.	No.	5.2e-08			
Matches	10	Mismatches	0	Indels	0	Gaps	0

RESULT 5  
 ADH35129  
 ID ADH35129 standard; peptide; 18 AA.  
 XX  
 AC ADH35129;  
 XX DT 11-MAR-2004 (first entry)  
 XX DE Complement c4 glycopeptide SEQ ID NO:18B.  
 KW identification; quantification; glycopolyptide; glycopeptide;  
 KW diagnostic marker; solid support; glycosylated polypeptide;  
 KW differential glycosylation; cancer; glycoprotein; characterisation;  
 KW diagnostic biomarker; immunotherapy; drug development; toxicology;  
 KW drug targeting.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX PN WO2003102018-A2.  
 XX PD 11-DEC-2003.  
 XX PR 03-JUN-2003; 2003WO-US017635.  
 XX PR 03-JUN-2002; 2002US-0385707P.  
 XX PR 09-MAY-2003; 2003US-0469361P.  
 PA (SYST-) INST SYSTEMS BIOLOGY.  
 XX PT Aebersold RH, Zhang H;  
 XX DR WPI; 2004-081931/08.  
 XX PT Identifying and quantifying glycopolyptides in sample by derivatizing  
 PT glycopolyptides, immobilizing and quantifying released glycopeptide  
 PT fragments.  
 XX PS Example 6; SEQ ID NO 18B; 162pp; English.  
 CC The present invention describes a method (M1) for identifying and  
 CC quantifying glycopolyptides (I) in a sample. M1 comprises derivatising  
 CC (I), immobilising the derivatised (I), cleaving the immobilised (I),  
 CC labelling the immobilised glycopeptide fragments (II) with an isotope  
 CC tag, releasing (III) from the solid support, analysing the released (III)  
 CC using mass spectrometry, identifying a released (II) and quantifying the  
 CC amount of (II). The method alternatively comprises: (a) immobilising (I)  
 CC to a solid support; (b) cleaving the immobilised (I); (c) labelling the  
 CC immobilised glycopeptides (III) with an isotope tag; and/or (c) releasing  
 CC (III) from the solid support; and (d) analysing the released (III). Also  
 CC described: (1) immobilising (M2) diagnostic marker for a disease,  
 CC comprising: (a) immobilising (I) from a test sample or control sample to  
 CC a first solid support or second solid support respectively; (b) cleaving  
 CC the immobilised (I); (c) labelling the immobilised (III) on the first and  
 CC second supports with differential isotope tags on the respective supports  
 CC ; (d) releasing (III) from the solid support; (e) analysing (III); and  
 CC (f) identifying one or more glycosylated polypeptides having differential  
 CC glycosylation between the test sample and the control sample; and (2) a  
 CC kit comprising a hydrazide resin, periodate and a pair of differentially  
 CC labelled isotope tags. (M1) is useful for identifying and quantifying (I)  
 CC in a sample and for identifying diagnostic marker for a disease such as  
 CC cancer. (M1) is useful for determining the sites of glycosylation, in the  
 CC determining changes in the abundance of glycoproteins and changes in the  
 CC state of glycosylation at individual glycosylation sites on those  
 CC glycoproteins that occur in response to perturbations of biological  
 CC systems and organisms in health and disease. (M1) is also useful for  
 CC purifying glycosylated proteins or peptides and for isolating and  
 CC identifying glycoproteins from the cell membrane or body fluids to  
 CC determine specific glycoprotein changes related to certain disease states  
 CC or cancer. (M1) is also useful for identifying, selecting and  
 CC characterising subgroups of carbohydrates and characterisation of  
 CC diagnostic biomarkers, immunotherapy and to evaluate the effectiveness of  
 CC drugs during development, optimal dosing, toxicology, drug targeting and  
 CC related therapeutic applications. The present sequence represents a  
 CC glycopeptide which is used in an example from the present invention.

RESULT 6  
 ADH35000  
 ID ADH35000 standard; peptide; 19 AA.  
 XX AC ADH35000;  
 XX DT 11-MAR-2004 (first entry)  
 XX DE N-linked glycopeptide #19.  
 XX PR 03-JUN-2003; 2003WO-US017635.  
 XX PR 03-JUN-2002; 2002US-0385707P.  
 XX PR 09-MAY-2003; 2003US-0469361P.  
 PA (SYST-) INST SYSTEMS BIOLOGY.  
 XX PT WO2003102018-A2.  
 XX PD 11-DEC-2003.  
 XX PR 03-JUN-2003; 2003WO-US017635.  
 XX PR 03-JUN-2002; 2002US-0385707P.  
 XX PR 09-MAY-2003; 2003US-0469361P.  
 PA (SYST-) INST SYSTEMS BIOLOGY.  
 XX PT WPI; 2004-081931/08.  
 XX PT Identifying and quantifying glycopolyptides in sample by derivatizing  
 PT glycopolyptides, immobilizing and quantifying released glycopeptide  
 PT fragments.  
 XX PS Example 15; FIG 28; 162pp; English.  
 CC The present invention describes a method (M1) for identifying and  
 CC quantifying glycopolyptides (I) in a sample. M1 comprises derivatising  
 CC (I), immobilising the derivatised (I), cleaving the immobilised (I),  
 CC labelling the immobilised glycopeptide fragments (II) with an isotope  
 CC tag, releasing (III) from the solid support, analysing the released (III)  
 CC using mass spectrometry, identifying a released (II) and quantifying the  
 CC amount of (II). The method alternatively comprises: (a) immobilising (I)  
 CC to a solid support; (b) cleaving the immobilised (I); (c) labelling the  
 CC immobilised glycopeptides (III) with an isotope tag; and/or (c) releasing  
 CC (III) from the solid support; and (d) analysing the released (III). Also  
 CC described: (1) identifying (M2) diagnostic marker for a disease,  
 CC comprising: (a) immobilising (I) from a test sample or control sample to  
 CC a first solid support or second solid support respectively; (b) cleaving  
 CC the immobilised (I); (c) labelling the immobilised (III) on the first and  
 CC second supports with differential isotope tags on the respective supports  
 CC ; (d) releasing (III) from the solid support; (e) analysing (III); and  
 CC (f) identifying one or more glycosylated polypeptides having differential  
 CC glycosylation between the test sample and the control sample; and (2) a

CC kit comprising a hydrazide resin, periodate and a pair of differentially  
 CC labelled isotope tags. (M1) is useful for identifying and quantifying (I)  
 CC in a sample and for identifying diagnostic marker for a disease such as  
 CC cancer. (M1) is useful for determining the sites of glycosylation,  
 CC determining changes in the abundance of glycoproteins and changes in the  
 CC state of glycosylation at individual glycosylation sites on those  
 CC glycoproteins that occur in response to perturbations of biological  
 CC systems and organisms in health and disease. (M1) is also useful for  
 CC purifying glycosylated proteins or peptides and for isolating and  
 CC identifying glycoproteins from the cell membrane or body fluids to  
 CC determine specific glycoprotein changes related to certain disease states  
 CC or cancer. (M1) is also useful for identifying, selecting and  
 CC characterising subgroups of carbohydrates and characterisation of  
 CC diagnostic biomarkers, immunotherapy and to evaluate the effectiveness of  
 CC drugs during development, optimal dosing, toxicology, drug targeting and  
 CC related therapeutic applications. The present sequence represents an N-  
 CC linked glycopeptide which is used in an example from the present  
 CC invention.

XX Sequence 19 AA:

Query Match 35.4%; Score 35; DB 8; Length 19;  
 Best local Similarity 63.6%; Pred. No. 2.6e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 7; Conservative 2;

Qy 2 SDGLWNNNQO 12  
 Db 3 SDGLESNSSTQ 13

XX

RESULT 7

ID ADC36109  
 XX ADC36109 standard; peptide; 12 AA.  
 AC ADC36109;

XX DT 18-DEC-2003 (first entry)

DB Chemokine binding peptide BKR-P143.

XX

KW peptidic chemokine modulator; antiinflammatory; antiallergic;  
 KW immunosuppressive; antidiabetic; antiarthritic; dermatological;  
 KW antiarthritic; antibacterial; antipsoriatic; antiseborrheic;  
 KW antiarteriosclerotic; hypotensive; neuroprotective; virutropic;  
 KW cytosolic; inflammation; allergy; immune response; autoimmune reaction;  
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;  
 KW allograft rejection; diabetes; sepsis; cancer; malignant cell growth;  
 KW acne; infection; arthritis; colitis; psoriasis; atherosclerosis;  
 KW hypertension; reperfusion ischaemia.

OS Synthetic.

XX

PN WO2003072599-A2.

XX

PD 04-SEP-2003.

XX

PP 27-FEB-2003; 2003WO-IL000155.

XX

PR 28-FEB-2002; 2002US-0359995P.

XX

PA (BIOK-) BIKINE THERAPEUTICS LTD.

XX

PI Peled A, Eisenberg O, Vaizel-Ohayon D;

XX

DR WPI; 2003-671869/63.

XX

PT New Peptidic chemokine modulator, useful for preparing a composition for  
 PT treating a disease modulated through and/or caused by binding of a  
 PT chemokine to a chemokine receptor, e.g., inflammation, diabetes, sepsis  
 PT or cancer.

XX

PS Example 1; Page 29; 43pp; English.

CC The present invention describes a peptidic chemokine modulator (I) for  
 CC modulating a biological effect of a chemokine. (I) comprises a molecule  
 CC consisting of: (a) the amino acids His, Ser, Ala, Leu, Ile, Lys, Arg, Thr  
 CC and Pro, and features at least 2 histidines spread along the molecule,  
 CC where the molecule features an overall positive charge (family 1); or (b)  
 CC the amino acids His, Pro, Thr, Leu, Arg and Trp and features at least two  
 CC neighbouring histidines, where the molecule features an overall positive  
 CC charge (family 2). Also described: (1) a composition for treating a  
 CC condition involving abnormal cell migration in a subject; (2) a method  
 CC for treating a disease modulated through and/or caused by binding of a  
 CC chemokine to a chemokine receptor in a subject; (3) an antibody for  
 CC binding to a chemokine-binding receptor that recognises at least a  
 CC portion of a chemokine-binding peptide; (4) a vaccine  
 CC formed with the antibody; and (5) a method for producing an antibody. (I)  
 CC has antiinflammatory, antiallergic, immunosuppressive, antidiabetic,  
 CC antirheumatic, dermatological, antiarthritic, antibacterial,  
 CC antipsoriatic, antiseborrheic, antiarteriosclerotic, hypotensive,  
 CC neuroprotective, virutropic and cytotoxic activities. The  
 CC peptidic chemokine modulator is useful for preparing a composition for  
 CC treating a disease modulated through and/or caused by binding of a  
 CC chemokine to a chemokine receptor comprising inflammation (primary or  
 CC secondary), allergy, a non-optimal immune response, an autoimmune  
 CC reaction (including rheumatoid arthritis, systemic lupus erythematosus,  
 CC multiple sclerosis and others), allograft rejection, diabetes, sepsis,  
 CC cancer and any type of malignant cell growth, acne and chronic bacterial  
 CC and viral infections, arthritis, colitis, psoriasis, atherosclerosis,  
 CC hypertension or reperfusion ischaemia. The present sequence represents a  
 CC chemokine binding peptide, which is used in an example from the present  
 CC invention.

XX Sequence 12 AA:

Query Match 34.3%; Score 34; DB 7; Length 12;  
 Best Local Similarity 71.4%; Pred. No. 2.2e+02; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 1;

Qy 6 WANNQO 12  
 Db 2 WNSNSTQ 8

XX

RESULT 8

ID ABU13471  
 ID ABU13471 standard; peptide; 19 AA.

AC ABU13471;

XX DT 21-FEB-2003 (first entry)

DB zona pellucida protein (ZP1) peptide #66.

XX

KW Human; zona pellucida; immunogen; ZP1; sperm; contraceptive; vaccine.

XX

OS Homo sapiens.

XX

PN US6455041-B1.

XX

PD 24-SEP-2002.

XX

PP 17-NOV-1999; 99US-00441502.

XX

PR 17-NOV-1998; 98US-0108822P.

XX

PA (DUMB/) DUNBAR B S.

XX

PI Dunbar BS;

XX

DR WPI; 2003-089265/08.

XX

PT Inducing anti-zona pellucida protein antibodies in a mammal, comprises  
 PT administering to the mammal one or more zona pellucida peptide.

XX

PS Example 1; Col 9; 33pp; English.

XX  
 CC This invention relates to a novel human anti-zona pellucida protein (ZP1)  
 CC antibodies in a mammal. The method comprises administering to the mammal  
 CC one or more zona pellucida peptides shown in the specification. The  
 CC invention also discloses a method for preventing sperm binding to zona  
 CC pellucida in a mammal, this may be used as a contraceptive or to create a  
 vaccine. The method of the invention is useful for inducing antibodies to  
 CC the zona pellucida protein, thus, resulting in a contraceptive effect in  
 multiple mammalian species. The present sequence represents a human zona  
 CC pellucida immunogenic peptide used to generate the specific antibodies of  
 the invention

XX  
 SQ Sequence 19 AA;  
 Query Match 34.3%; Score 34; DB 6; Length 19;  
 Best Local Similarity 53.8%; Pred. No. 3.7e+02;  
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 SSDGLWNWNTQL 13  
 Db 1 SGSGIGDNYOTQL 13

RESULT 9  
 ABP83017  
 ID ABP83017 standard; peptide; 20 AA.

XX  
 AC ABP83017;  
 XX  
 DT 04-MAR-2003 (first entry)

XX  
 DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1690.  
 XX  
 KW G protein-coupled receptor; GPCR; antigenic Peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261087-A2.

XX  
 PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US050107.

PR 19-DEC-2000; 2000US-0257144P.

XX  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX  
 PI Burmer GC, Roush CL, Brown JP;

XX  
 DR WPI; 2003-046718/04.

XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.

XX  
 PS Claim 1; Fig 2; 523pp; English.

XX  
 CC The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP86119) of 12-24 amino  
 acids. Also described: (1) an assay for the detection of a particular G  
 protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or

CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 antibody against a particular GPCR, and in the production of specific  
 antibodies. The peptides and antibodies are also useful for detecting the  
 presence or absence of corresponding GPCRs. The antigenic peptides for  
 GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 regeneration-related disease, immunological-related cell proliferative  
 diseases or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode  
 CC GPCR proteins given in ABP1675 to ABP82018, which are used in the  
 CC exemplification of the present invention

XX  
 SQ Sequence 20 AA;  
 Query Match 34.3%; Score 34; DB 6; Length 20;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 SSDGLWNWNN 9  
 Db 12 SSSSNWNWN 20

RESULT 10  
 ADEB1136  
 ID ADB1136 standard; peptide; 18 AA.

XX  
 AC ADEB1136;  
 XX  
 DT 29-JAN-2004 (first entry)

DE Antigenic peptide B1-92-109 #SEQ ID 18.

XX  
 KW Antigenic Peptide; omega-oxidation; fatty acid; alkane; alpha;  
 KW omega-dicarboxylic acid; yeast; antibody; perfume; polymer; adhesive;  
 KW macrocide antibiotic.

XX  
 OS Candida tropicalis.

XX  
 PN WO2003089611-A2.

XX  
 PD 30-OCT-2003.

XX  
 PR 18-APR-2003; 2003WO-US012158.

XX  
 PR 19-APR-2002; 2002US-0074066P.

XX  
 PR 18-APR-2003; 2003US-00418820.

XX  
 PA (COGN-) COGNIS CORP.

XX  
 PI Zhang Y, Wilson CR;

XX  
 WPI; 2004-011692/01.

XX  
 PS Claim 1; SEQ ID NO 18; 66pp; English.

XX  
 CC The invention relates to antigenic peptides having any of seven specific  
 CC sequences (of 16-25 amino acids, reproduced) or their analogs,  
 CC derivatives and immunologically active fragments. They are used to raise  
 CC antibodies (Ab) that bind selectively to enzymes (II) involved in the

CC omega-oxidation of fatty acids or alkanes to alpha,omega-dicarboxylic  
 CC acids in yeast. Antigenic peptides are used to raise antibodies (Ab)  
 CC specific for yeast enzymes (II) involved in the omega-oxidation of fatty  
 CC acids or alkanes to alpha,omega-dicarboxylic acids (III). Antibodies are  
 CC used to detect/quantify (III), especially for monitoring their induction  
 CC and/or stability during oxidation to (III), e.g. for manipulating (II)  
 CC for increased yield of (III), and also to verify the effect of  
 CC modifications of yeast enzyme encoding genes. Alpha,omega-dicarboxylic  
 CC acids are useful as intermediates for perfumes, polymers, adhesives and  
 CC macrolide antibiotics. The current sequence represents an antigenic  
 CC peptide designed for recombinant antibody generation.

SQ Sequence 18 AA:

Query Match 33.3%; Score 33; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 5;  
 Matches 5; Conservative 0; Indels 0; Gaps 0;

QY 4 GLWNN 8  
 Db 1 GLWNN 5

RESULT 11

ABG8087 33.3%; Score 33; DB 8; Length 18;  
 ID ABG8087 Standard; protein; 20 AA.

XX AC ABG8087;  
 XX DT 29-NOV-2002 (first entry)

DE Human esf mutant protein E107N.  
 XX KW Scaffold Protein; C-type lectin-like domain; CTL<sup>D</sup>; alpha-helix;

KW beta-strand; connecting segment; 14loop region; tetratracetin;  
 KW ligand-binding specificity; human; mouse; rat; chicken; murine; mutein.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX PN WO200248189-A2.

XX PD 20-JUN-2002.  
 XX PR 13-DEC-2001; 2001WO-DK000825.

XX PR 13-DEC-2000; 2000DK-00001872.  
 PR 28-FEB-2001; 2001US-0272098P.

XX PA (BORÉ-) BOREAN PHARMA AS.

PI Etzerodt M, Holter TL, Graversen NJH, Thøgersen HC;  
 XX DR WPI; 2002-643278/69.

XX PT Protein comprising a variant of model C-type lectin-like domains (CTL<sup>D</sup>),  
 PT in which alpha helices, beta-strands, connecting segments are conserved  
 PT to maintain CTL<sup>D</sup> scaffold structure, while the loop region is altered.  
 XX PS Claim 1; Page 19; 168pp; English.

CC The present invention relates to a new protein with scaffold structure of  
 CC C-type lectin-like domains (CTL<sup>D</sup>). The invention comprises a variant of a  
 CC model CTL<sup>D</sup> where alpha-helices and beta-strands and connecting segments  
 CC are conserved such that scaffold structure of C-type lectin-like domains  
 CC (CTL<sup>D</sup>) is substantially maintained, while the 14loop region is altered by  
 CC amino acid substitution, deletion, insertion or their combination. The  
 CC invention is useful for preparing a library of nucleotide sequences  
 CC encoding related proteins by randomising part or all of the nucleic acid  
 CC sequence encoding the loop region of its CTL<sup>D</sup>. The artificial CTL<sup>D</sup>  
 CC protein products are preferable to antibody derivatives as each binding  
 CC site is a single structurally autonomous protein domain. When used as  
 CC components of compositions to be used for in vivo diagnostic or

CC therapeutic purposes, artificial CTL<sup>D</sup> protein products constructed on the  
 CC basis of human CTL<sup>D</sup>s are virtually identical to the corresponding natural  
 CC CTL<sup>D</sup> protein already present in the body and are therefore less  
 CC immunogenic to the patient. They also have a smaller size, and thus  
 CC provide tissue penetration and distribution, as well as shorter half life  
 CC in circulation. Since murine and human tetratracetin are identical in  
 CC structure, straightforward swapping of polypeptide segments defining  
 CC ligand-binding specificity between murine and human tetratracetin  
 CC derivatives may be achieved. The present amino acid sequence represents a  
 CC mutant protein of the invention

SQ Sequence 20 AA:

Query Match 33.3%; Score 33; DB 5; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 5.5e+02; Mismatches 4;  
 Matches 4; Conservative 3; Indels 0; Gaps 0;

QY 4 GLWNNNN 10  
 Db 13 GMWNNDNR 19

RESULT 12

ABO14120 33.3%; Score 33; DB 5; Length 20;  
 ID ABO14120 Standard; peptide; 20 AA.

XX AC ABO14120;  
 XX DT 21-AUG-2003 (first entry)

DE Novel human secreted protein fragment #21.  
 XX Human; secreted protein; cytosstatic; neuroprotective; hepatotropic;  
 KW gene therapy; cancer; liver disorder; hepatitis; neural disorder;  
 KW Alzheimer's disease.

OS Homo sapiens.  
 OS Synthetic.  
 XX PN US2003028003-A1.

XX FD 06-FEB-2003.  
 XX PR 12-OCT-2001; 2001US-00974879.

XX PR 07-NOV-1997; 97US-0054900P.  
 PR 07-NOV-1997; 97US-0064908P.

PR 07-NOV-1997; 97US-0064911P.  
 PR 07-NOV-1997; 97US-0064912P.

PR 07-NOV-1997; 97US-0064933P.  
 PR 07-NOV-1997; 97US-0064984P.

PR 07-NOV-1997; 97US-0064985P.  
 PR 07-NOV-1997; 97US-0064977P.

PR 07-NOV-1997; 97US-0064988P.  
 PR 07-NOV-1997; 97US-0066089P.

PR 17-NOV-1997; 97US-0066090P.  
 PR 17-NOV-1997; 97US-0066094P.

PR 17-NOV-1997; 97US-0066095P.  
 PR 17-NOV-1997; 97US-0066100P.

PR 04-NOV-1997; 98WO-US023435.  
 PR 05-MAY-1999; 99US-00305736.  
 PR 13-OCT-2000; 2000US-0229893P.  
 PR 28-MAR-2001; 2001US-00818683.

XX PA (ROSE/) ROSEN C A.  
 PA (FENG/) FENG P.  
 PA (RUBB/) RUBEN S M.  
 PA (EBUR/) EBNER R.  
 PA (OLSEN/) OLSEN H S.

PA (NIUJ/) NI J.  
 PA (WEI Y) WEI Y.  
 PA (SOPP/) SOPPET D R.  
 PA (MOOR/) MOORE P A.  
 PA (KYAW/) KYAW H.

PA (LAFLU/) LAFLEUR D W.  
 PA (SHTY/) SHI Y.  
 PA (JANAT/) JANAT F.  
 PA (ENDR/) ENDRESS G A.  
 PA (CART/) CARTER K C.  
 PA (BIRSE/) BIRSE C E.  
 XX  
 PI Rosen CA, Feng P, Ruben SM, Ebner R, Olsen HS, Ni J, Wei Y;  
 PI Soppet DR, Moore PA, Kyaw H, Lafleur DW, Shi Y, Janat F;  
 PI Endress GA, Carter KC, Birse CE;  
 XX  
 DR WPI; 2003-479549/45.

XX  
 PT New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disease.  
 PT  
 XX  
 PS Disclosure; Page 9; 496pp; English.

CC The invention describes a new isolated nucleic acid molecule comprising a sequence having at least 95% identity with a sequence comprising: (a) a polynucleotide (PN) fragment of a sequence comprising 420-3435 bp, or its allelic variant; (b) a PN fragment of the cDNA sequence; (c) a PN sequence encoding a polypeptide, or its fragment, domain, epitope or species homologue; or (d) a PN that hybridizes under stringent conditions to any one of the sequences of (A)-(C). The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disease. This is the amino acid sequence of a novel human secreted protein fragment

CC Sequence 20 AA;

Query Match 33.3%; Score 33; DB 6; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 5.5e+02; Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 Qy 5 LWNNTQTLREHS 18  
 Db | ||||| | : :  
 5 LVTNNQTQLQEAE 18

RESULT 13  
 ADG78515  
 ID ADG78515 standard; peptide; 20 AA.

AC  
 XX  
 DT 11-MAR-2004 (first entry)

DE Human secreted protein #138.

XX  
 KW Human; secreted protein; immune disorder; haematopoietic disorder; hyperproliferative disorder; infectious disease; inflammatory disorder; HIV; anaemia; thrombocytopoenia; bleeding; stroke; myocardial infarction; Addison's disease; rheumatoid arthritis; dermatitis; Grave's disease; multiple sclerosis; glomerulonephritis; diabetes; graft-versus-host disease; graft-versus-host disease; inflammatory bowel disease; cancer; bacterial infection; viral infection; parasitic infection; osteoporosis; wound; atherosclerosis; Alzheimer's disease; Parkinson's disease; ulcer; food additive; food preservative.

XX  
 OS Homo sapiens.

XX  
 PN US2003211472-A1.

XX  
 PD 13-NOV-2003.

XX  
 PF 28-MAR-2001; 2001US-00818683.

XX  
 PR 05-MAY-1999; 99US-00305736.

PA (FENG/) FENG P.  
 PA (RUBEN/) RUBEN S.  
 PA (ROSE/) ROSEN C A.  
 PA (EBNER/) EBNER R.  
 PA (OLSEN/) OLSEN H S.  
 PA (NIU/) NI J.  
 PA (WEI/) WEI Y.  
 PA (SOPP/) SOPPET D R.  
 PA (MOOR/) MOORE P A.  
 PA (KYAW/) KYAW H.  
 PA (LAFLU/) LAFLEUR D W.  
 PA (SHIY/) SHI Y.  
 PA (JANAT/) JANAT F.  
 PA (ENDR/) ENDRESS G A.  
 PA (CART/) CARTER K C.  
 XX  
 DR WPI; 2004-051575/05.

XX  
 PT New secreted nucleic acid for diagnosing, preventing or treating diseases associated with aberrant expression or activity of the polypeptide it encodes, e.g. cancer, human immunodeficiency virus, Parkinson's disease, PT or diabetes.

XX  
 RS Disclosure; SEQ ID NO 276; 377pp; English.

CC The invention also relates to human secreted proteins and the nucleic acids encoding them. The proteins and nucleic acids are useful in diagnosing, preventing, prognosis or treating diseases or disorders associated with aberrant expression and/or activity of the secreted proteins, such as immune disorders, haematopoietic disorders, hyperproliferative disorders, infectious diseases or inflammatory disorders. In particular, the diseases or disorders are HIV, anaemia, thrombocytopenia, bleeding, stroke, myocardial infarction, Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease, multiple sclerosis, glomerulonephritis, diabetes, graft-versus host disease, inflammatory bowel disease, cancer, bacterial infections, viral infections, parasitic infections, osteoporosis, wounds, atherosclerosis, Alzheimer's disease, Parkinson's disease or ulcers. The sequences may also be used as food additives or preservatives, or for modulating mammalian mental or physical characteristics. The nucleic acids are also used in chromosome mapping, in forensic biology or as molecular weight markers. This sequence represents a human secreted protein of the CC invention.

XX  
 SQ Sequence 20 AA;

Query Match 33.3%; Score 33; DB 8; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 5.5e+02; Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 Qy 5 LWNNTQTLREHS 18  
 Db | ||||| | : :  
 5 LVTNNQTQLQEAE 18

RESULT 14  
 ADN60818  
 ID ADN60818 standard; peptide; 20 AA.

XX  
 AC ADN60818;  
 XX  
 DT 01-JUL-2004 (first entry)

DE Human secreted polypeptide #149.

XX  
 KW Human; secreted polypeptide; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast; liver; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; nervous system disorder; Alzheimer's disease;







CC and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the T cells, a T cell clone or a T cell population or preparation is useful for identifying heteroclitic epitopes or for preparing a composition for treating HCV infection. The present sequence represents a synthetic peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match Best Local Similarity 31.3%; Score 31; DB 8; Length 15; Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGLWNWNTQL 13  
Db 2 NTNGSWHINNTAL 14

RESULT 21

ID ADL25931 Standard; peptide; 15 AA.

AC ADL25931;

XX DT 17-JUN-2004 (first entry)

DB Synthetic peptide A118 derived from a conserved region of HCV.

XX KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA; major histocompatibility complex; human leukocyte antigen.

OS Synthetic.

XX PN WO2004024182-A2.

XX PD 25-MAR-2004.

XX PP 27-AUG-2003; 2003WO-EP009482.

XX PR 13-SEP-2002; 2002AT-00001376.

PR 27-FEB-2003; 2003WO-EP002005.

PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Buschle M, Habel A, Klade C, Mattnar F, Otava O, Vyrvyska O; PI Zauner W, Zinke S, Kirlappos H;

XX DR WPI; 2004-269899/25.

PT Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the PT molecule by separating the complex from the HCV-peptides which do not bind to the molecule.

XX PS Example 1; Page 30; 73PP; English.

XX CC The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (Hps). The method of the invention has virucide activity, CC and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (Hps) which have a binding capacity CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T CC cells, a T cell clone or a T cell population or preparation is useful for identifying heteroclitic epitopes or for preparing a composition for CC treating HCV infection. The present sequence represents a synthetic peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match Best Local Similarity 38.5%; Score 31; DB 8; Length 15; Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGLWNWNTQL 13  
Db 2 NTNGSWHINNTAL 15

RESULT 22

ID ADL25933 Standard; peptide; 15 AA.

AC ADL25933;

XX DT 17-JUN-2004 (first entry)

DB Synthetic peptide A120 derived from a conserved region of HCV.

XX KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA; major histocompatibility complex; human leukocyte antigen.

OS Synthetic.

XX PN WO2004024182-A2.

XX PD 25-MAR-2004.

XX PP 27-AUG-2003; 2003WO-EP009482.

XX PR 13-SEP-2002; 2002AT-00001376.

PR 27-FEB-2003; 2003WO-EP002005.

PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Buschle M, Habel A, Klade C, Mattnar F, Otava O, Vyrvyska O; PI Zauner W, Zinke S, Kirlappos H;

XX DR WPI; 2004-269899/25.

PT Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the PT molecule by separating the complex from the HCV-peptides which do not bind to the molecule.

XX PS Example 1; Page 30; 73PP; English.

XX CC The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (Hps). The method of the invention has virucide activity, CC and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (Hps) which have a binding capacity CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T CC cells, a T cell clone or a T cell population or preparation is useful for identifying heteroclitic epitopes or for preparing a composition for CC treating HCV infection. The present sequence represents a synthetic peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match Best Local Similarity 38.5%; Score 31; DB 8; Length 15; Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGLWNWNTQL 13  
Db 2 NTNGSWHINNTAL 13

RESULT 23

ID ADL25932 Standard; peptide; 15 AA.



New hepatitis C virus (HCV) peptides and mosaic antigen composition comprising the peptides, useful as immunoreagents for detecting HCV antibodies infection, or as an immunogen for stimulating production of antibodies against HCV.

PS  
 XX  
 CC  
 CC The present sequence is that of peptide MDL-16 comprising amino acid residues 412-429 of the hepatitis C virus (HCV) polyprotein E2 region. A panel of HCV polyprotein-derived peptides was tested for immunoreactivity with a commercially available human serum panel. All of the immunoreactivity was concentrated within the core region between amino acids 1 to 80. MDL-16 exhibited low and inconsistent immunogenicity. The invention provides a highly immunoreactive mosaic antigen composition, (MAC) comprising 2 or more HCV immunoreactive peptides (see AAM0816-27), each of which is immobilized to a carrier. The unique combination of HCV core peptides in the MAC provides higher specificity and sensitivity for detection of human antibodies specificity to HCV in rapid HCV diagnostic applications. An in vitro diagnostic method for detecting anti-HCV antibodies in a test sample and a diagnostic test kit are provided which use the MAC as an immunoreagent. The HCV MAC may also potentially be used as an immunogen in vaccine compositions. (Updated on 07-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 17 AA;

	Query Match	Score	Length	DB	Mismatches	Pred.	No.	Indels	Gaps
QY	1 SSDGILWNNQTOI	31	31	5	5	9.3e+02	3	0	0
Db	4 NTTNGSSWHIRNTAL	31	16						

RESULT 26  
 ABW01700  
 ID ABW01700 standard; protein; 19 AA.  
 XX  
 AC ABW01700;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Toxoplasma gondii TATI-1 transacting factor activation domain.  
 KW Cellular vaccine; tetracycline repressor; TetR; transacting factor;  
 KW protozoal infection; gene therapy; TATI.  
 XX  
 OS Toxoplasma gondii.  
 PN US2003185851-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 20-MAR-2002; 2002US-00102143.  
 XX  
 PR 20-MAR-2002; 2002US-00102143.  
 XX  
 PA (SOLDI/) SOLDATI D.  
 PA (MEIS/) MEISSNER M.  
 XX  
 PI Soldati D, Meissner M;  
 XX  
 DR WPI; 2003-844144/78.  
 DR N-PSDB; AAD63241.  
 XX  
 PT Nucleic acid and cellular vaccines useful for treating protozoal  
 PT infections caused by e.g. Toxoplasma gondii and Plasmodium falciparum.  
 PS Disclosure; FIG 6A; OPP; English.  
 XX  
 CC The present invention relates to nucleic acid and cellular vaccines which

XX SQ Sequence 19 AA;

Query Match 31.3%; Score 31; DB 7; Length 19;  
Best Local Similarity 60.0%; Pred. No. 1.e+03;保守性 0; Mismatches 0; Indels 0; Gaps 0;

Matches	6; Conservative	0; Mismatches	4; Indels	0; Gaps	0;
Qy	6 WNNNOTOLPL	15			
Db	8 WNNIQPYLGL	17			

RESULT 28

ADA26471 ADA26471 standard; peptide; 20 AA.

XX AC ADA26471;

XX DT 20-NOV-2003 (first entry)

XX DE Isomaltose manufacture method enzyme-derived peptide #19.

XX KW isomaltose; alpha-isomaltosyl gluco-sugar synthase; alpha-1; 4-glucosyl bond; isomaltitol;

XX KW alpha-isomaltosyl glucosugar; alpha-1; 6-glucosyl bond; isomaltose; health food; beverage; fodder; cosmetic; pharmaceutical; humectant; osmotic pressure regulators; sugar crystallization inhibitor; starch aging inhibitor.

XX OS Sporosarcina globispora.

XX PN WO2003033717-A1.

XX PD 24-APR-2003.

XX PF 18-OCT-2002; 2002WO-JP010846.

XX PR 18-OCT-2001; 2001JP-00321182.

XX PR 30-AUG-2002; 2002JP-00252609.

XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX PI Kubota M, Nishimoto T, Sonoda T, Fukuda S, Miyake T;

XX DR WPI; 2003-430348/40.

XX PT Manufacture of isomaltose in two-step process from specified sugar types using specified enzymes, for manufacture of isomaltitol and use in foodstuffs, fodder, pharmaceuticals and cosmetics.

XX PS Disclosure; Page 205; 260pp; Japanese.

XX The invention relates to the manufacture of isomaltose by making one or more alpha-isomaltosyl gluco-sugar synthase from *Bacillus globisporus* N75 (FERM BP-7591), *Arthrobacter globiformis* Al9 (FERM BP-7590) and *Arthrobacter ramosus* Sl (FERM BP-7592), in the presence or absence of alpha-isomaltosyl transferase from *Bacillus globisporus* N75 (FERM BP-7591) and/or *Arthrobacter globiformis* Al9 (FERM BP-7590) act on a sugar of glucose polymerization degree of two or more having alpha-1,4-glucosyl bonds as the bonding of the non-reducing terminal to give a alpha-isomaltosylglucosugar with glucose polymerization degree of three or more having a alpha-1,6-glucosyl bond as a non-reducing terminal and alpha-1,4 -glucosyl bonds as the other terminals and/or cyclol-6)-alpha-D-glucopyranosyl-(1-3)-alpha-D-glucopyranosyl-(1-1), acting on this with isomaltose release enzyme and collecting the isomaltose. The isomaltose and isomaltitol are used in health foods and beverages, fodder and feeds, cosmetics and pharmaceuticals, and luxury articles, as humectant, osmotic pressure regulators, low sweetness, sugar crystallization inhibitor, and starch aging inhibitors. This sequence represents a peptide derived from one of the above proteins.

XX Sequence 20 AA;

Query Match 31.3%; Score 31; DB 6; Length 20;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;保守性 4; Mismatches 0; Indels 0; Gaps 0;

Matches	3 DGLMN	8
Qy	3   :	
Db	4 DGWHN	9

RESULT 29

ADH80940 ADH80940 standard; peptide; 20 AA.

XX AC ADH80940;

XX DT 15-APR-2004 (first entry)

XX DE HIV hypervariable epitope construct (HEV) #5.

XX KW antimicrobial; vaccine; immunogenic peptide mixture; immunogenic epitope; pathogen; reactive immunity; human immunodeficiency virus; HIV; hypervariable epitope construct.

XX OS Human immunodeficiency virus 1.

XX KEY Location/Qualifiers

FT Misc-difference 11 /note= "Thr, Ser"

FT FT Note= "Ile, Thr"

PT 05-DEC-2002.

XX PF 08-FEB-2002; 2002US-00072084.

XX PR 09-OCT-1998; 98US-0103642P.

PR 08-OCT-1999; 99US-00414484.

XX PA (TORR/) TORRES J V.

XX PI Torres JV;

XX DR WPI; 2003-328635/31.

XX PT Preparation of immunogenic peptide mixtures for e.g. producing vaccines, by obtaining immunogenic epitope sequences having common residue regions and variable residues, and determining frequency of amino acids at the PT variable residues.

XX PS Example 1; Fig 3; 30pp; English.

XX CC The invention describes the preparation of an immunogenic peptide mixture. The mixture is prepared by obtaining immunogenic epitope sequences of a pathogen having a common residue region and at least one variable residue, determining the frequency with which different amino acids are found at the variable residue and synthesising a peptide mixture comprising up to 100 different peptides using the amino acids. the peptide mixture is useful in the production of vaccines, therapeutic agents and diagnostic kits against pathogenic organisms, e.g. viruses and parasites. The inventive method produces less complex immunogenic peptide formulation than those described in the prior art, while retaining optimum immunogenicity. The resulting immunogenic peptide mixture evokes broadly reactive immunity. This is the amino acid sequence of a human immunodeficiency virus type 1 hypervariable epitope construct used in the immunogenic peptide mixture of the invention.

XX SQ Sequence 20 AA;

Query Match 31.3%; Score 31; DB 7; Length 20;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03;



Query Match 31.3%; Score 31; DB 8; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 1.1e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 NNNNOTLFLIE 16  
 Db 6 NYNQNQLIME 15

RESULT 32

ADE8906 standard; Peptide; 10 AA.

ID ADE8906;  
 AC XX  
 DT 29-JAN-2004 (first entry)

DE Interleukin 13 receptor subunit alpha 2 immunogenic peptide.  
 XX immune response; interleukin 13 receptor subunit alpha 2; IL-13Ralpha2;  
 KW anti-cancer; vaccine; human; immunogenic.  
 XX Synthetic  
 OS Homo Sapiens.  
 XX WO2003092717-A1.

XX 13-NOV-2003.

XX 22-MAR-2002; 2002WO-US008983.

XX 22-MAR-2002; 2002WO-US008983.

XX (PENN-) PENN STATE RES FOUND.

XX Debinski W, Christensen N, Mintz A;  
 PI XX WPI: 2003-903570/82.

XX PT Stimulating an immune response against IL-13Ralpha2 in a subject having  
 PT or at risk for developing a disease, e.g., cancer, by formulating an anti-  
 PT cancer vaccine comprising an agent that can stimulate the immune response  
 PT against.

PS Example 3; Page 43; 67pp; English.  
 XX  
 CC The present invention describes a method for stimulating an immune  
 response against Interleukin 13 receptor subunit alpha 2 (IL-13alpha2)  
 CC in a subject having or at risk for developing a disease having cells  
 expressing IL-13Ralpha2. The method comprises formulating an anti-cancer  
 vaccine comprising an agent that can stimulate an immune response against  
 CC IL-13Ralpha2 when administered to an animal, outside of the subject; and  
 administering the vaccine to the subject to stimulate an immune response  
 against IL-13Ralpha2 in the subject. Also described: (1) a composition  
 for stimulating the immune response against IL-13Ralpha2 when  
 administered to an animal comprising an isolated gene that can stimulate  
 an immune response against IL-13Ralpha2 when administered to the animal,  
 and carrier; (2) a method for directing an antibody to cells expressing  
 CC IL-13Ralpha2 in a subject by formulating a pharmaceutical composition  
 outside of a subject, where the composition comprises an antibody that  
 specifically binds IL-13Ralpha2 and a carrier; and administering the  
 pharmaceutical composition to the subject to allow the antibody to  
 specifically bind to the cells expressing IL-13Ralpha2 in the subject;  
 CC and (3) a pharmaceutical composition comprising the antibody that  
 specifically binds IL-13Ralpha2 and a carrier. The methods and  
 composition are useful for stimulating an immune response against IL-  
 13Ralpha2 in a subject having or at risk for developing a disease having  
 CC cells expressing IL-13Ralpha2. The present sequence represents an  
 immunogenic peptide for IL-13Ralpha2, which is used in an example from  
 CC the present invention.

Query Match 30.3%; Score 30; DB 7; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 7.5e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSDGLWN 7  
 Db 2 SDDGWS 8

RESULT 33

AAE10548 standard; peptide; 12 AA.

ID AAE10548;  
 AC XX  
 DT 10-DEC-2001 (first entry)

DE Llama species antibody VH CDR3 #17.  
 XX Llama antibody; camelid; anorectics; heavy chain variable domain; VH;  
 KW human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL;  
 KW food; human gastric lipase; HGL; cosmetic control; body weight;  
 KW complementarity determining region 3; CDR3.  
 XX OS Lama sp.  
 XX EP1134231-A1.  
 XX PD 19-SER-2001.  
 XX BP 20-FEB-2001; 2001EP-00200703.  
 XX PR 14-MAR-2000; 2000EP-00200930.  
 XX PA (UNIL ) UNILEVER NV.  
 PA (UNIL ) UNILEVER PLC.  
 XX DR Bezemer S, Van De Burg M, De Haard JMW, Tareilus E;  
 XX WPI; 2001-572718/65.

PT New antibody or its fragments for inhibiting human dietary enzymes,  
 PT useful for cosmetic control of body weight of human beings, comprises  
 PT heavy chain variable domain derived from immunoglobulin naturally devoid  
 PT of light chains.

PS Claim 4; Page 29; 37pp; English.

XX The patent discloses antibodies or their fragments comprising a heavy  
 CC chain variable domain (VHH) derived from an immunoglobulin naturally  
 CC devoid of light chain specific for inhibiting human dietary enzymes. The  
 CC antibodies of the invention are useful for the preparation of medicaments  
 CC or food for inhibiting the activity of one or more human dietary enzymes  
 especially human pancreatic lipase (HPL) or human gastric lipase (HGL)  
 CC which are useful for the cosmetic control of body weight of human beings.  
 CC The present peptide sequence is a complementarity determining region 3  
 (CDR3) of llama species (camelid) antibody VH region  
 XX SQ Sequence 12 AA:

Query Match 30.3%; Score 30; DB 4; Length 12;  
 Best Local Similarity 62.5%; Pred. No. 9.1e+02; Mismatches 5; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSDGLWN 8  
 Db 4 SYDGWSND 11

RESULT 34

ABB80837 standard; protein; 12 AA.

SQ Sequence 10 AA;

AC	ABB0837;	PR	12-AUG-1999; 99US-0148935P.
XX	DT	XX	23-SEP-2002 (first entry)
XX	DE	XX	Heparin binding laminin alpha4 protein fragment.
KW	XX	XX	Laminin alpha4; heparin; signal transduction; transgenic; cancer; angiogenesis; cytostatic; vasotropin; gene therapy; mouse.
OS	XX	XX	Mus musculus.
PN	XX	XX	WO200249349-A1.
PD	XX	XX	20-JUN-2002.
PF	XX	XX	10-JUL-2001; 2001WO-JP005976.
PR	XX	XX	12-DEC-2000; 20000JP-0037899.
PA	XX	XX	(KYOWA ) KYOWA HAKKO KOGYO KK.
PT	XX	XX	Kitagawa Y, Shitara K, Ohki Y;
PI	XX	XX	WPI; 2002-490604/52.
DR	XX	XX	Polypeptides binding strongly to heparin for treatment of cancer and angiogenesis-related disorders.
PT	XX	XX	Example: Page 106; 129pp; Japanese.
PS	XX	XX	The invention relates to a polypeptide forming part of the laminin alpha4 chain G domain, having molecular weight below 108 kDa, and capable of binding to heparin. The polypeptide can be used to inhibit heparin-binding signal transduction from cells. The polypeptide, encoding DNA, non-human transgenic animals and transgenic plants containing the recombinant DNA can all be used for the treatment and prevention of cancer and angiogenesis-related diseases. The present sequence represents a fragment of the heparin binding mouse laminin alpha4 protein sequence 12 AA;
SQ	Query Match 30.3%; Score 30; DB 5; Length 12; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;	SEQ ID 2 SDGLMNN 8	Query Match 30.3%; Score 30; DB 5; Length 14; Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	XX	QY	XX
Db	XX	Db	XX
RESULT 35	AAB73315	RESULT 36	AAB73315 standard; peptide; 14 AA.
AC	AAB73315;	AC	ID ABU0795 standard; peptide; 14 AA.
XX	DT 22-MAY-2001 (first entry)	XX	DT 05-SEP-2002 (first entry)
XX	DE Human PC-LECTIN extracellular domain peptide, SEQ ID NO:25.	XX	DE Human PC-LECTIN; C-type lectin; transmembrane antigen; normal testis; Human; PC-LECTIN; C-type lectin; transmembrane antigen; normal testis; laylvin homologue; prostate cancer antigen; overexpression; androgen-dependent prostate cancer; diagnosis; prognosis; extracellular domain; antigenic; antibody. Homo sapiens.
XX	XX	XX	Human; PC-LECTIN; C-type lectin; transmembrane antigen; normal testis; laylvin homologue; prostate cancer antigen; overexpression; androgen-dependent prostate cancer; diagnosis; prognosis; extracellular domain; antigenic; antibody. Homo sapiens.
XX	XX	XX	Human; PC-LECTIN; C-type lectin; transmembrane antigen; normal testis; laylvin homologue; prostate cancer antigen; overexpression; androgen-dependent prostate cancer; diagnosis; prognosis; extracellular domain; antigenic; antibody. Homo sapiens.
XX	XX	XX	Human; PC-LECTIN; C-type lectin; transmembrane antigen; normal testis; laylvin homologue; prostate cancer antigen; overexpression; androgen-dependent prostate cancer; diagnosis; prognosis; extracellular domain; antigenic; antibody. Homo sapiens.
XX	XX	XX	B lymphocyte affinity maturation library peptide #69.
KW	XX	XX	B lymphocyte stimulator protein binding protein; Blys; immune disease; allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinemia; blood clotting; ischaemia; graft-versus-host disease; neurodegenerative disease; immunosuppressive; nephrotic; anti-rheumatic; antiarthritic; neuroprotective; cytosolic; immunomodulant; antitumour; anti-HIV; antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic; dermatological; antiinflammatory; cardiotonic; ophthalmological; uropathic; antidiabetic; anithyroid; antidepressant; hepatotropic.
OS	XX	XX	WO200112811-A1.
PN	XX	XX	22-FEB-2001.
PD	XX	XX	11-AUG-2000; 20000WO-US022065.

XX  
OS Unidentified.  
XX  
PN WO200216411-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025850.  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B Lymphocyte Stimulator binding polypeptide.  
XX  
PR Claim 70; Page 215; 38pp; English.  
XX  
CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production; B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
SQ Sequence 14 AA;  
Query Match 30.3%; Score 30; DB 5; Length 14;  
Best Local Similarity 38.5%; Pred. No. 1.1e+03;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
QY 5 LWNNNOTQFLER 17  
Db :|:|:|:  
2 IWDPLTKMLPH 14  
RESULT 38  
ID AAR85392  
ID AAR85392 standard; peptide; 15 AA.  
XX  
AC AAR85392;  
XX  
DT 13-JUN-1996 (first entry)  
XX  
DB HTLV-IIIB envelope glycoprotein antigenic peptide, SP-15.  
XX  
KW Human immunodeficiency virus; HIV; HTLV-IIIB; envelope; glycoprotein;  
KW hydrophobic; immunisation; antibody production; fusion peptide; SP-1;  
KW conjugate; carrier.  
XX  
OS Synthetic.  
XX  
PN W09529700-A1.  
XX  
PD 09-NOV-1995.  
XX  
PR 28-APR-1995; 95WO-US005465.  
XX  
PR 29-APR-1994; 94US-00235305.  
XX  
PA (UWU-) UNIV DUKE.  
XX  
PI Haynes BF, Parker TJ;  
XX  
WPI; 1995-392926/50.  
XX  
DR New peptide(s) corresponding to HIV sequences - used for inducing  
PT protective immunity to HIV and in the treatment of e.g. auto-immune  
PT disease, infectious disease or tumours.  
XX  
PS Example 1; Page 42; 128pp; English.  
XX  
CC AAR85388-R8593 synthetic peptides with hydrophilic amino acid sequences  
CC of the HIV isolate HTLV-IIIB envelope protein.These peptides can be  
CC covalently linked to a carrier molecule. The conjugate produced is  
capable of inducing the production of high titres of protective, type-

CC specific; anti-HIV antibodies. Helper T cells and cytotoxic T cells are  
 CC also activated by the peptide immunogens  
 XX  
 SQ Sequence 15 AA;

Query Match	30.3%; Score 30; DB 2; Length 15;
Qy	Best local similarity 41.7%; Pred No. 1.2e+03; Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Db	4 DGLMWNQDQLF 14 4 DGGNSNNESEIF 15

RESULT 39  
 AAWI9031  
 ID AAWI9031 standard; peptide; 15 AA.  
 XX  
 AC AAWI9031;  
 XX  
 DT 16-JAN-1998 (first entry)  
 XX  
 DE SP-15 region of HIV envelope glycoprotein.  
 XX  
 KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;  
 KW recognition; B lymphocyte; type specific; antibody; vaccine; protection;  
 KW immune response; infection; neutralisation; SP-15 region.  
 OS Human immunodeficiency virus.  
 XX  
 PN WO9714436-A1.  
 XX  
 PD 24-APR-1997.  
 XX  
 PP 18-OCT-1996; 96WO-US016911.  
 XX  
 PR 20-OCT-1995; 95US-00546515.  
 PR 09-FEB-1996; 96US-0059266.  
 PA (UYDU-) UNIV DUKE.  
 PI Haymes BF, Parker TJ;  
 DR WPI; 1997-244862/22.  
 XX  
 PT synthetic human immunodeficiency virus vaccine - comprising hydrophilic  
 PT peptide corresponding to at least 1 antigenic determinant of envelope  
 PT glyco:protein recognised by B lymphocytes.  
 XX  
 PS Example 1; Page 37; 104pp; English.

XX  
 CC An essentially pure hydrophilic peptide, comprising at least 1 antigenic  
 CC determinant of human immunodeficiency virus (HIV) envelope (env)  
 CC glycoprotein (gp) recognised by B lymphocytes, i.e. the present sequence,  
 CC when covalently linked to a carrier molecule, induces the production of  
 CC high titre of protective, type specific anti-HIV antibodies (Ab) in  
 CC mammal. The peptide can be used in vaccines for producing a protective  
 CC immune response to HIV infection, while a HIV neutralising Ab can be  
 CC induced in a primate by administering a composition comprising HIV env  
 XX  
 SQ Sequence 15 AA;

Query Match 30.3%; Score 30; DB 8; Length 15;  
 Best Local Similarity 41.7%; Pred No. 1.2e+03; Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Query Match	30.3%; Score 30; DB 8; Length 15;
Qy	Best local similarity 41.7%; Pred No. 1.2e+03; Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Db	2 SDGLWNQDQL 13 1 TNGSWHINRTL 12

Search completed: December 30, 2004, 16:28:14  
 Job time : 160 secs

GenCore version 5.1.6  
Copyright (C) 1993 - 2004 Compugen Ltd.



**RESULT 4**

S09334 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
 transcobalamin I precursor - pig (fragment)  
 N;Alternate names: haptocorrin  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
 C;Accession: S09334  
 R;Hewitt, J.B.; Seetharam, B.; Leykam, J.; Alpers, D.H.  
 Eur.-J. Biochem., 189, 125-130, 1990  
 A;Title: Isolation and characterization of a cDNA encoding porcine gastric haptocorrin.  
 A;Reference number: S09334; MUID:90235848; PMID:2331993  
 A;Accession: S09334  
 A;Molecule type: mRNA  
 A;Residues: 1-416 <HEW>  
 A;Cross-references: UNIPROT:P17630; EMBL:X52566; NID:91963; PID:CAA36800.1; PID:g1964  
 C;Superfamily: gastric intrinsic factor  
 C;Keywords: glycoprotein  
 F;1-24/Domain: signal sequence (fragment) #status predicted <SNT>  
 F;25-416/Product: haptocorrin #status predicted <MTS>  
 Query Match 48 5%; Score 48; DB 2; Length 416;  
 Best Local Similarity 44.4%; Pred. No. 6.3;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 Qy 1 SSDGLWNQNOTQFLHHS 18  
 Db 378 SVQGTVWANNRERTYWEHS 395

**RESULT 5**

JQ1978  
 structural polyprotein - Venezuelan equine encephalitis virus (subtype II, strain Evergl  
 N;Contains: 6K protein; coat protein; membrane glycoprotein E1; membrane glycoprotein E2  
 C;Species: Venezuelan equine encephalitis virus  
 C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
 C;Accession: JQ1978  
 R;Sneider, J.M.; Kinney, R.M.; Tsuchiya, K.R.; Trent, D.W.  
 J. Gen. Virol., 74, 519-523, 1993  
 A;Title: Molecular evidence that epizootic Venezuelan equine encephalitis (VEE) I-AB vir  
 A;Reference number: JQ1978; MUID:93187617; PMID:8445371  
 A;Accession: JQ1978  
 A;Molecule type: mRNA  
 A;Residues: 1-1254 <SNT>  
 C;Cross-references: UNIPROT:P36330; GB:104598; NID:9290612; PID:AAA42984.1; PID:g290614  
 C;Superfamily: togavirus structural polyprotein  
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F;1-274/Product: coat protein #status predicted <CTP>  
 F;275-333/Product: membrane glycoprotein E2 #status predicted <E2>  
 F;334-756/Product: membrane glycoprotein E2 #status predicted <MG3>  
 F;701-721/Domain: transmembrane #status predicted <TM1>  
 F;757-812/Product: 6K protein #status predicted <KP6>  
 F;794-813/Domain: transmembrane #status predicted <TM2>  
 F;813-1254/Product: membrane glycoprotein E1 #status predicted <MG1>  
 F;1233-1248/Domain: transmembrane #status predicted <TM3>  
 F;47,285,545,651,946/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 48 5%; Score 48; DB 1; Length 1254;  
 Best Local Similarity 57.9%; Pred. No. 21;  
 Matches 11; Conservative 1; Mismatches 3; Indels 4; Gaps 1;  
 Qy 1 SSDGLWNQNOTQFLHHS 15  
 Db 762 SLDDHLWNQNOTQFLHHS 780

**RESULT 6**

VHWWTE  
 structural polyprotein - Venezuelan equine encephalitis virus (strain TC-83)  
 N;Contains: 6K peptide; coat protein; membrane glycoprotein E1; membrane glycoprotein E2  
 C;Species: Venezuelan equine encephalitis virus  
 C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 09-Jul-2004  
 C;Accession: A27871  
 R;Johnson, B.J.B.; Kinney, R.M.; Kost, C.L.; Trent, D.W.

**RESULT 7**

VHWWVTT  
 structural polyprotein - Venezuelan equine encephalitis virus (strain TRD)  
 N;Contains: 6K protein; coat protein; membrane glycoprotein E1; membrane glycoprotein E2  
 C;Species: Venezuelan equine encephalitis virus  
 C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C;Accession: B31467; A47612  
 R;Kinney, R.M.; Johnson, B.J.B.; Welch, J.B.; Tsuchiya, K.R.; Trent, D.W.  
 R;Kinney, R.M.; Johnson, B.J.B.; Welch, J.B.; Tsuchiya, K.R.; Trent, D.W.  
 A;Title: The full-length nucleotide sequences of the virulent Trinidad donkey strain of  
 A;Reference number: A31467; MUID:89243175; PMID:2524126  
 A;Accession: B31467  
 A;Molecule type: mRNA  
 A;Residues: 1-1254 <K11>  
 A;Cross-references: UNIPROT:P09592; GB:J04332; NID:9323708; PID:AAB02519.1; PID:g323710  
 R;Kinney, R.M.; Johnson, B.J.B.; Brown, V.L.; Trent, D.W.  
 Virology, 152, 400-413, 1986  
 F;275-333/Domain: transmembrane #status predicted <TM1>  
 F;701-718/Domain: transmembrane #status predicted <TM2>  
 A;Molecule type: mRNA  
 A;Residues: 1-542, 'K', 544-810, 'P', 812-1254 <K12>  
 A;Cross-references: GB:01442  
 C;Superfamily: togavirus structural polyprotein  
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F;1-275/Product: coat protein #status predicted <CTP>  
 F;276-334/Product: membrane glycoprotein E3 #status predicted <MG3>  
 F;335-757/Product: membrane glycoprotein E2 #status predicted <MG2>  
 F;701-718/Domain: transmembrane #status predicted <TM1>  
 F;774-790/Domain: transmembrane #status predicted <TM2>  
 F;795-813/Domain: transmembrane #status predicted <TM3>  
 F;813-1248/Product: membrane glycoprotein E1 #status predicted <MG1>  
 F;1233-1248/Domain: transmembrane #status predicted <TM4>  
 F;47,285,546,652,946/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 48 5%; Score 48; DB 1; Length 1254;  
 Best Local Similarity 50.0%; Pred. No. 21;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SSDGLWNQNOTQFLHHS 16  
 Db 763 SLDDHLWNQNOTQFLHHS 778

RESULT 8

B44213 structural polyprotein - Venezuelan equine encephalitis virus (strain P676) DNA (cytosine-5')-methyltransferase (EC 2.1.1.37) T6G15.160 - Arabidopsis thaliana  
 Contains: 6K protein; coat protein; membrane glycoprotein E1; membrane glycoprotein E2  
 C;Species: Venezuelan equine encephalitis virus (strain P676)  
 C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
 C;Accession: B44213  
 R;Kinney, R.M.; Tauchira, K.R.; Sneider, J.M.; Trent, D.W.  
 Virology 191, 569-580, 1992  
 A;Title: Genetic evidence that epizootic Venezuelan equine encephalitis (VEE) viruses ma  
 A;Reference number: A44213; MUID:93079859; PMID:1446915  
 A;Accession: B44213  
 A;Molecule type: genomic RNA  
 A;Residues: 1-1255 <KIN>  
 A;Cross-references: UNIPROT:P36332; GB:L04653; NID:9290609; PIDN: AAC19319.1; PID:9290611  
 C;Superfamily: togavirus structural polyprotein  
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F;1-275-/Product: coat protein #status predicted <CTP>  
 F;276-334-/Product: membrane glycoprotein E3 #status predicted <MG3>  
 F;335-757-/Product: membrane glycoprotein E2 #status predicted <MG2>  
 F;702-722-/Domain: transmembrane #status predicted <TM1>  
 F;758-813-/Product: 6K protein #status predicted <KP6>  
 F;814-1255-/Product: membrane glycoprotein E1 #status predicted <MG1>  
 F;1232-1249-/Domain: transmembrane #status predicted <TM2>  
 F;47, 286, 652, 947-/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match  
 Best Local Similarity 50.0%; Score 48; DB 1; Length 1255;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 SDGIGIWNNTQTLIE 16  
 Db 763 SLDHLWNNNQQMENWQ 778

RESULT 9

D44213 structural polyprotein - Venezuelan equine encephalitis virus (strain 3880) DNA (cytosine-5')-methyltransferase; S-adenosylmethionine  
 C;Species: Venezuelan equine encephalitis virus (strain 3880)  
 C;Accession: D44213  
 C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
 C;Accession: D44213  
 R;Kinney, R.M.; Tauchira, K.R.; Sneider, J.M.; Trent, D.W.  
 Virology 191, 569-580, 1992  
 A;Title: Genetic evidence that epizootic Venezuelan equine encephalitis (VEE) viruses ma  
 A;Reference number: A44213; MUID:93079859; PMID:1446915  
 A;Accession: D44213  
 A;Molecule type: genomic RNA  
 A;Residues: 1-1255 <KIN>  
 A;Cross-references: UNIPROT:P36329; GB:L00930; NID:9323706; PIDN: AAC19325.1; PID:9137509  
 C;Superfamily: togavirus structural polyprotein  
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F;1-275-/Product: coat protein #status predicted <CTP>  
 F;276-334-/Product: membrane glycoprotein E3 #status predicted <MG3>  
 F;335-757-/Product: membrane glycoprotein E2 #status predicted <MG2>  
 F;702-722-/Domain: transmembrane #status predicted <TM1>  
 F;758-813-/Product: 6K protein #status predicted <KP6>  
 F;795-814-/Domain: transmembrane #status predicted <TM2>  
 F;814-1255-/Product: membrane glycoprotein E1 #status predicted <MG1>  
 F;1232-1249-/Domain: transmembrane #status predicted <TM2>  
 F;47, 286, 652, 947-/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match  
 Best Local Similarity 50.0%; Pred. No. 21; length 1255;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 SDGIGIWNNTQTLIE 16  
 Db 763 SLDHLWNNNQQMENWQ 778

RESULT 10

T06663 DNA (cytosine-5')-methyltransferase (EC 2.1.1.37) T6G15.160 - Arabidopsis thaliana  
 N;Alternate name: protein T6G15.160  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Accession: T06663  
 R;Heaven, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X  
 submitted to the Protein Sequence Database, April 1999  
 A;Reference number: ZL15791  
 A;Accession: T06663  
 A;Molecule type: DNA  
 A;Residues: 1-1404 <BEV>  
 A;Cross-references: UNIPROT:Q9TQ11; EMBL:AL049556; GSPDB:GN00062; ATSP:T6G15.160  
 A;Experimental source: cultivar Columbia; BAC clone T6G15  
 C;Genetics:  
 A;Gene: AISP-T6G15.160  
 A;Map position: 4  
 A;introns: 57/1; 348/3; 371/2; 872/3; 927/3; 989/1; 1026/2; 1086/3; 1152/3; 1245/3; 1288/  
 C;Keywords: methyltransferase; S-adenosylmethionine  
 A;Experimental source: cultivar Columbia; BAC clone T6G15  
 Query Match  
 Best Local Similarity 47.5%; Score 47; DB 2; Length 1404;  
 Matches 8; Conservative 57.1%; Pred. No. 35; 2; Mismatches 4; Indels 0; Gaps 0;  
 Qy 2 SDGLMNNTQTLIE 15  
 Db 1095 SDGSWSKQQCQML 1108

RESULT 11

S46008 probable carboxypeptidase C (EC 3.4.16.5) YBR139w - Yeast (Saccharomyces cerevisiae)  
 NT;Alternate names: hypothetical protein YBR1015; hypothetical protein YBR139w  
 C;Species: Saccharomyces cerevisiae  
 C;Accession: S46008; S46581  
 C;Date: 26-Aug-1994 #sequence\_revision 05-Jan-1996 #text\_change 16-Aug-2004  
 C;Accession: S46008; S46581  
 R;Bacan, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.  
 Submitted to the Protein Sequence Database, August 1994  
 A;Reference number: S45995  
 A;Accession: S46008  
 A;Molecule type: DNA  
 A;Residues: 1-508 <BBC>  
 A;Cross-references: UNIPROT:P38109; EMBL:236008; NID:9536435; PIDN:CAA85097.1; PID:9536454  
 A;Experimental source: strain S288C  
 R;Bacan, A.M.; Cullin, C.; Grzybowska, E.; Lacroute, F.; Nasr, F.; Ozier-Kalogeropoulos,  
 Yeast 10 (Suppl. A), S1-S11, 1994  
 A;Title: The sequence of 29.7-kb from the right arm of chromosome II reveals 13 complete c  
 A;Reference number: S46569; MUID:94378717; PMID:8091856  
 A;Accession: S46581  
 A;Molecule type: DNA  
 A;Residues: 1-508 <BBC>  
 A;Cross-references: EMBL:X75891; NID:9496856; PIDN:CAA53497.1; PID:9496869  
 A;Experimental source: strain S288C  
 C;Genetics:  
 A;Cross-references: SGD:S0000343  
 A;Map position: 2R  
 A;Note: MIPS YBR139w  
 C;Superfamily: Serine carboxypeptidase  
 C;Keywords: hydrolase; serine carboxypeptidase; transmembrane protein  
 F;6-22-/domain: transmembrane #status predicted <TM6>  
 F;29, 415, 474-/Active site: Ser, Asp, His #status predicted  
 Query Match  
 Best Local Similarity 63.6%; Score 46; DB 1; Length 508;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 6 WNNNTQTLIE 16  
 Db 160 WNNNNSMIFLE 170

RESULT 12

A86445 unknown protein [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: A86445  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Hulzar, L.  
 Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzali, R.; Rooney, T.; Rowley, D.; Sakano, H.  
 Rizzo, M.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: A86445  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-230 <S>TO>  
 A;Cross-references: UNIPROT:Q9C6X3; GB:AE005172; NID:g10092437; PIDN:AAG12841.1; GSPDB:Q  
 C;Genetics:  
 A;Map position: 1

RESULT 13  
 LNRT2  
 hepatic lectin 2 - rat  
 N;Alternate name: asialoglycoprotein receptor RHL-2/3 (ASGP-R2/3)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 31-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 09-Jul-2004  
 C;Accession: B28462; A28462; A31601; A26888; A53417  
 R;Halberg, D.F.; Wager, R.E.; Farrell, D.C.; Hildreth IV, J.; Quesenberry, M.S.; Loeb, J.J. Biol. Chem. 262, 9828-9938, 1987  
 A;Title: Major and minor forms of the rat liver asialoglycoprotein receptor are independent of Reference number: A28462; MUID:8725056; PMID:3597443  
 A;Accession: B28462  
 A;Cross-references: UNIPROT:P08290; GB:J02762; NID:g205162; PIDN:AAA41522.1; PID:g205163  
 A;Molecule type: mRNA  
 A;Residues: 1-301 <HAL>  
 A;Accession: A28462  
 A;Molecule type: protein  
 A;Residues: 88-361, 'X', 98-118, 'X', 120-129-158;177-182, 'X', 184, 'X', 186-189, 192-290, 'C', 292  
 R;Sanford, J.P.; Elliot, R.W.; Doyle, D.  
 DNA 7, 721-728, 1986  
 A;Title: Asialoglycoprotein receptor genes are linked on chromosome 11 in the mouse.  
 A;Reference number: A31601; MUID:8970119; PMID:3234778  
 A;Accession: A31601  
 A;Molecule type: mRNA  
 A;Residues: 1-301 <SAN>  
 A;Cross-references: GB:X07636; NID:g57066; PIDN:CAA30476.1; PID:g57067  
 R;McPhee, M.; Berg, P.  
 Mol. Cell. Biol. 7, 1841-1847, 1987  
 A;Accession: A26888  
 A;Reference number: A26888; MUID:87257885; PMID:3600647  
 A;Molecule type: mRNA  
 A;Residues: 1-122  
 A;Cross-references: GB:MI6347; NID:g906649; PIDN:AA42038.1; PID:g906649  
 A;Title: Identification and characterization of cDNA clones encoding two homologous proteins  
 A;Note: the authors translated the codon GCA for residue 153 as Arg and ATT for residue  
 R;Drickamer, K.; Mamom, J.F.; Blums, G.; Leung, J.O.  
 J. Biol. Chem. 259, 770-778, 1984  
 A;Title: Primary structure of the rat liver asialoglycoprotein receptor: structural evidence  
 A;Reference number: A25417; MUID:84111554; PMID:6319386

Query Match 45.5%; Score 45; DB 1; Length 301;  
 Best Local Similarity 72.7%; Pred. No. 13; 2; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 2;

Qy	2 SDGLIMNNNQTO 12
Db	276 SDGLWWDNFQO 286

RESULT 14  
 S29159 glutamate receptor, NMDA-sensitive, epsilon-1 chain precursor - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: S29159  
 R;Meguro, H.; Mori, H.; Araki, K.; Kushiyama, E.; Kutsuwada, T.; Yamazaki, M.; Kumanishi, N.; Nature 357, 70-74, 1992  
 A;Title: Functional characterization of a heteromeric NMDA receptor channel expressed f.  
 A;Reference number: S29159; MUID:9224461; PMID:1374164  
 A;Accession: S29159  
 A;Molecule type: mRNA  
 A;Residues: 1-1464 <MEG>  
 A;Cross-references: UNIPROT:P35436; EMBL:D10217; NID:g220410; PID:BA01069.1; PID:g220  
 C;Superfamily: N-methyl-D-aspartate receptor 2A; glutamate receptor homology  
 C;Keywords: ion channel; neurotransmitter receptor; transmembrane protein  
 F;1-19:Domain: signal sequence #status predicted <SIG>  
 F;20-1464:Product: glutamate receptor epsilon-1 chain #status predicted <MAT>  
 F;428-854:Domain: transmembrane #status predicted <TM1>  
 F;557-576:Domain: transmembrane #status predicted <TM2>  
 F;599-618:Domain: transmembrane #status predicted <TM3>  
 F;629-647:Domain: transmembrane #status predicted <TM4>  
 F;817-837:Domain: transmembrane #status predicted <TM4>  
 Query Match 45.5%; Score 45; DB 1; Length 1464;  
 Best Local Similarity 47.1%; Pred. No. 76; 2; Indels 0; Gaps 0;  
 Matches 8; Conservative 5; Mismatches 4; DB 1174 NEDGLPNNDQKLYAKH 1190  
 Qy 1 SSDGLIMNNNQTOFLFEEH 17  
 Db 1174 NEDGLPNNDQKLYAKH 1190

RESULT 15  
 A43274 N-methyl D-aspartate receptor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 31-Dec-1993 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
 C;Accession: A43274; A45219  
 R;Monyer, H.; Sprengel, R.; Schoepfer, R.; Herb, A.; Higuchi, M.; Lomeli, H.; Burnashev, N.; Science 256, 1217-1221, 1992  
 A;Title: Heteromeric NMDA receptors: molecular and functional distinction of subtypes.  
 A;Reference number: A43274; MUID:92271257; PMID:1350383  
 A;Accession: A43274  
 A;Molecule type: DNA  
 A;Residues: 1-1464 <MON>  
 A;Experimental source: brain  
 A;Note: sequence modified after extraction from NCBI backbone  
 J;Ishii, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa, C.; Biol. Chem. 268, 2836-2843, 1993  
 A;Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor  
 A;Reference number: A45219; MUID:9315502; PMID:8428958



A:Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonist  
A:Accession number: S01114; MUID:88296835; PMID:1342060  
A:Molecule type: DNA  
A:Cross-references: UNIPROT:P11483; EMBL:X12712; NID:91861; PIDN:CAA31215.1; PID:91862  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane; G-protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane  
F:68-91/Domain: transmembrane #status predicted <TM1>  
F:105-125/Domain: transmembrane #status predicted <TM2>  
F:143-164/Domain: transmembrane #status predicted <TM3>  
F:185-207/Domain: transmembrane #status predicted <TM4>  
F:231-252/Domain: transmembrane #status predicted <TM5>  
F:493-513/Domain: transmembrane #status predicted <TM6>  
F:528-546/Domain: transmembrane #status predicted <TM7>  
F:528-546/Domain: transmembrane #status predicted <TM7>

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps	Matches	Conservative	1	Mismatches	8	Indels	0	Gaps	0	
Qy	1	SSDCIWNWNNTOLFLEHS	18					Db	332	SSSDSWNNDAAASLENS	349						

**RESULT 20**  
SA:7572  
muscarinic acetylcholine receptor m3 - bovine  
C:Species: Bos primigenius taurinus (cattle)  
C:Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S47572  
Rihee, P.H.K.; Hedges, P.K.; Glickman, F.; Chang, K.J.  
Biochem. Biophys. Acta 1223, 151-154, 1994  
A:Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 receptor  
A:Reference number: S47572; MUID:94339178; PMID:8861048  
A:Accession: S47572  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-590 <LEE>  
A:Cross-references: UNIPROT:P41994; EMBL:U08286; NID:9520465; PIDN:AAA51866.1; PID:95204  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: neurotransmitter receptor

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps	Matches	Conservative	1	Mismatches	8	Indels	0	Gaps	0
Qy	1	SSPGLWNWNNTOLFLEHS	18					Db	332	SSSDSWNNDAAASLENS	349					

**RESULT 21**  
A55019  
muscarinic acetylcholine receptor, M3 isoform - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A55019  
R.Gadbut, A.P.; Galper, J.B.  
J. Biol. Chem. 269, 25823-25829, 1994  
A:Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and atrioventricular node  
A:Reference number: A55019; MUID:95014393; PMID:7929287  
A:Accession: A55019  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-639 <GAD>  
A:Cross-references: UNIPROT:P49578; GB:L10617; NID:9530097; PIDN:AAA65961.1; PID:9530098  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: neurotransmitter receptor

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps	Matches	Conservative	1	Mismatches	8	Indels	0	Gaps	0
Qy	1	SSPGLWNWNNTOLFLEHS	18					Db	332	SSSDSWNNDAAASLENS	349					

RESULT 22

QY	'1SSPQIWNQTOFLEHS 18									
T35238	T35238 .::        ::									
C.Species	Streptomyces coelicolor									
C.Date	05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004									
C.Accession	T35238									
R.Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.										
Submitted to the EMBL Data Library, September 1998										
A.Reference number:	Z21572									
A;Accession:	T35238									
A.Status:	preliminary; translated from GB/EMBL/DDJB									
A.Residues:	1-973 <SEE>									
A;Cross-references:	UniProt:O86728; EMBL:AL031515; PIDN:CAA20643.1; GSPDB:GN00070; SCOEDB									
A;Experimental source:	strain A3(2)									
C;Genetics:										
A;Gene:	SCOEDB:SC5C7.31C									
Query Match      Score 44; DB 2; Length 973;										
Best Local Similarity 63.6%; Pred. No. 70; Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;										
QY	3 DGLWNENNQTL 13									
Db	872 DGMWBNNQDAL 882									

RESULT 23

GBCE										
beta-D-galactosidase (EC 3.2.1.23) alpha chain - Escherichia coli (strain K-12)										
N;Alternate names:	beta-D-galactoside galactohydrolyase; lactase; phospho-beta-D-galactosidase; Escherichia coli									
C.Species	Escherichia coli									
C.Date	30-Sep-1987 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004									
C.Accession	A65996; R25751; S09206									
R.Blaettner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co										
A.; Rose, D.J.; Mau, B.; Shao, Y.										
Science 277, 1455-1462, 1997										
A.Title:	The complete genome sequence of Escherichia coli K-12.									
A.Reference number:	A64720; MURP:97426617; PMID:9288503									
A;Accession:	A65996									
A.Status:	nucleic acid sequence not shown; translation not shown									
A.Molecule type:	DNA									
A;Residues:	1-1042 <BLAT>									
A;Cross-references:	UniProt:P05864; UniProt:Q47170; GB:AE000389; GB:U00096; NID:91789451									
A;Experimental source:	strain K-12, substrate MG1655									
R.Stokes, H.W.; Betts, P.W.; Hall, B.G.										
Mol. Biol. Evol. 2, 469-477, 1985										
A.Title:	Sequence of the ebgA gene of Escherichia coli: comparison with the lacZ gene.									
A;Reference number:	A93056; MURP:88216133; PMID:3939707									
A;Accession:	A2551									
A.Molecule type:	DNA									
A;Residues:	80-476, 'R', 478-651, 'S', 653-660, 'P', 662-674, 'CRSWTPAKRS', 685-724, 'KCASV', 730-									
A;Cross-references:	GB:X03228; GB:MI3700; GB:MI3796; NID:941311; PIDN:CAA26978.1; PID:94									
R.Fowler, A.V.; Smith, P.J.										
J. Biol. Chem. 258, 10204-10207, 1983										
A.Title:	The active site regions of lacZ and ebg beta-galactosidases are homologous.									
A.Reference number:	A92390; MURP:8329932; PMID:6411710									
A;Contents:	annotation; active site regions									
R.Hall, B.G.; Betts, P.W.; Wootton, J.C.										
Genetics 123, 635-648, 1989										
A.Title:	DNA sequence analysis of artificially evolved ebg enzyme and ebg repressor gene									
A;Reference:	S09205; MURP:90128218; PMID:2515108									
A;Accession:	S09206									
A;Molecule type:	DNA									
A;Residues:	13-476, 'R', 478-651, 'S', 653-660, 'P', 662-779, 'M', 780-1037, 'T', 1039-1042 <HAL>									
A;Cross-references:	EMBL:203031; NID:941307; PIDN:CDA36724.1; PID:941309									
C;Comment:	The wild-type enzyme is an ineffective lactase. Two classes of point mutation:									

C;Genetics:  
A;Gene: ebga  
A;Map position: 68 min  
C;Complex: homohexamer  
C;Superfamily: beta-galactosidase  
C;Keywords: glycosidase; hexamer; hydrolase; magnesium  
F'413, 415, 461; Binding site: Glu, Tyr, Glu #status predicted  
P'461, 502, 524/Active site: Glu, Tyr, Glu #status predicted

Query Match 44.4%; Score 44; DB 1; Length 1042;  
Best Local Similarity 46.7%; Pred. No. 76;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 DGLMANNNQTQFLEH 17  
Db 788 EGLWQPNHLQIMQEH 802

RESULT 24

E85668 evolved beta-D-galactosidase alpha subunit [imported] - Escherichia coli (strain 0157:H7)

C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: E85968  
R;Perma\_N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, I.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimaranta, E.; Potamitis, K.; Apodaca, Nature 409, 529-533, 2001.  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: E85968  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1042 <STO>  
A;Cross-references: UNIPROT:Q8XAM9; GB:AE005174; NID:912517660; PIDN:AAG58209.1; GSPDB:Q  
A;Experimental source: strain 0157:H7, substrain EDL033  
C;Genetics:  
A;Gene: ebga  
C;Superfamily: beta-galactosidase

Query Match 44.4%; Score 44; DB 2; Length 1042;  
Best Local Similarity 46.7%; Pred. No. 76;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 DGLMANNNQTQFLEH 17  
Db 788 EGLWQPNHLQIMQEH 802

RESULT 25

F91123 evolved beta-D-galactosidase alpha subunit [imported] - Escherichia coli (strain 0157:H7)

C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: F91123  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurikawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gabbara, N.; Yasunaga, T.; Kuwara, S.; Shiba, T.; Hattori, M.; Shinawa, H. DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic reference number: A96929; MUID:21156231; PMID:11258796  
A;Accession: F91123  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1042 <HAY>  
A;Cross-references: UNIPROT:Q8XAM9; GB:BA000007; PIDN:BAB37381.1; PIDN:913363431; GSPDB:Q  
A;Experimental source: strain 0157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: EC8395B  
C;Superfamily: beta-galactosidase

Query Match 44.4%; Score 44; DB 2; Length 1042;  
Best Local Similarity 46.7%; Pred. No. 76;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 DGLMANNNQTQFLEH 17  
Db 788 EGLWQPNHLQIMQEH 802

RESULT 26

C82931 hypothetical protein UU126 [imported] - Ureaplasma urealyticum

C;Species: Ureaplasma urealyticum  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C;Accession: C82931  
R;Glass, J.I.; Leffkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chan, E.Y.; Cassell, G.H. submitted to GenBank, February 2000  
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor A;Reference number: A82870  
A;Accession: C82931  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1084 <GLA>  
A;Cross-references: GB:AE002113; GB:AF222994; NID:96899078; PIDN:AAF30532.1; GSPDB:GN001;  
A;Experimental source: Serovar 3; biovar 1  
C;Genetics:  
A;Gene: UU126  
A;Genetic code: SGCG3  
Query Match 44.4%; Score 44; DB 2; Length 1084;  
Best Local Similarity 50.0%; Pred. No. 79;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LWNNNQTQFLEHS 18  
Db 479 LWASQNQNLYLSDY 492

RESULT 27

S76938 hypothetical protein - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 16-Aug-2004  
C;Accession: S76938  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okamura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S76938  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-254 <KAN>  
A;Cross-references: UNIPROT:P74730; EMBL:990917; GB:AB001339; NID:91653036; PIDN:BA1895C  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C;Superfamily: ATP-binding cassette homology  
C;Keywords: ATP; nucleotide binding; P-loop  
P';45-65/Domain: nucleotide-binding cassette homology <ABC>  
P';62-69/Region: nucleotide-binding motif A (P-loop)

Query Match 43.4%; Score 43; DB 2; Length 254;  
Best Local Similarity 50.0%; Pred. No. 23;  
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 DGLMANNNQTQFLEHS 18  
Db 193 DKLWQHNTILVWSHS 208

RESULT 28

AG2598 conserved hypothetical protein phng [imported] - Agrobacterium tumefaciens (strain C58, 1)

C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 12-Jul-2004  
C;Accession: AG2598

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.F.; Chen, Y.; Woo, L.; Erage, G.; Gillett, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, J.; Kamp, P.; Romero, P.; Zhang, S.

Science 294, 2217-2223, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreepan, W.; Perry, M.; Gordon-Kamm, A.E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:1743193

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-153 <KUR>

A;Cross-references: UNIPROT:Q8UIW0; GB:AB008688; PIDN:HAL41205.1; PID:g17738507; GSPDB:G

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: phnG

A;Map position: circular chromosome

C;Superfamily: carbon-phosphorus lyase, component PhnG

Query Match 42.4%; Score 42; DB 2; Length 153;

Best Local Similarity 50.0%; Pred. No. 19;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DGLWNWNNOTQLFILE 16

Db 103 DALWQESQTRQPIE 116

RESULT 29

H97380

phnG protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 12-Jul-2004

C;Accession: H97380

A;Goodner, B.; Hinkle, G.; Alltung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Goldman, R.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Happas, C.; Markelz, B.; Science 294, 2223-2228, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: H97380

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-153 <KAY>

A;Cross-references: UNIPROT:Q8X613; GB:BA000007; PIDN:BAB37127.1; PID:g13363176; GSPDB:G

A;Experimental source: strain O157:H7, substrate RIMD 0509552

C;Genetics:

A;Gene: ECs3704

Query Match 42.4%; Score 42; DB 2; Length 269;

Best Local Similarity 58.3%; Pred. No. 35;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LWNNNOTQLFILE 16

Db 173 LWNNNQPKPPFK 184

RESULT 30

H65067

hypothetical protein b2847 - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C;Accession: H65067

A;Blaettner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C*c*, A.; Rose, D.J.; Mai, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-269 <BLAT>

RESULT 31

H91091

probable sensory transducer [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509552)

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C;Accession: H91091

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Kasavara, N.; Yasunaga, T.; Kuwara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

A;Title: Complete Genome Sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic features

A;Reference number: A99629; MUID:21156231; PMID:12128796

A;Accession: H91091

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-269 <HAY>

A;Cross-references: UNIPROT:Q8X613; GB:BA000007; PIDN:BAB37127.1; PID:g13363176; GSPDB:G

A;Experimental source: strain O157:H7, substrate RIMD 0509552

C;Genetics:

A;Gene: ECs3704

Query Match 42.4%; Score 42; DB 2; Length 269;

Best Local Similarity 58.3%; Pred. No. 35;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LWNNNOTQLFILE 16

Db 173 LWNNNQPKPPFK 184

RESULT 32

C85937

probable sensory transducer yqeI [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509552)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C;Accession: C85937

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mai, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimaranta, E.; Potamitis, K.; Apodaca, Nature 405, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: C85937

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-269 <STO>

A;Cross-references: UNIPROT:Q8X613; GB:AB005174; PIDN:g12517339; PIDN:AAG357959.1; GSPDB:G

A;Experimental source: strain O157:H7, substrate EDL933

C;Genetics:

A;Gene: yqeI

Query Match 42.4%; Score 42; DB 2; Length 269;

Best Local Similarity 58.3%; Pred. No. 35;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LWNNNOTQLFILE 16

Db 173 LWNNNQPKPPFK 184

RESULT 33

S73153

hypothetical protein 10 - red alga (Porphyra purpurea) chloroplast

C;Species: chloroplast *Porphyra purpurea*  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-440 <KRE>  
A;Cross-references: UNIPROT:P51232; EMBL:U38804; NID:gi1276652; PID:gi1276698  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995  
C;Gene: ycf10  
A;Genome: chloroplast  
C;Superfamily: maize chloroplast protein cemA  
C;Keywords: chloroplast

RESULT 34

Query Match	Best Local Similarity	Score	DB	Length
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	42.4%	42	2	278

Qy 3 DGLWNWNNOTQFLFHS 18  
Db 85 DYLMWNEQOPKIFINS 100

VGXR37

Query Match

Best Local Similarity	Score	DB	Length
43.8%; Pred. No. 36; Mismatches 6; Indels 0; Gaps 0;	42	2	278

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

C;Species: human rotavirus A  
C;Date: 30-Jun-1999 #sequence\_revision 30-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: C27620  
RiGreen, K.Y.; Midtthun, K.; Gorzeglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.; F  
Virology 161, 153-159, 1987  
A;Title: Comparison of the amino acid sequences of the major neutralization protein of f  
A;Reference number: A27620; MUID:8804489; PMID:2823458  
A;Accession: C27620  
A;Molecule type: genomic RNA  
A;Residues: 1-326 <GRE>  
A;Cross-references: UNIPROT:PI1852  
C;GeneticB:  
A;Map position: segment 9  
C;Superfamily: rotavirus glycoprotein VP7  
C;Keywords: coat protein; glycoprotein; transmembrane protein  
P:1-23-Domain: signal sequence #status predicted <SIG>  
F:2-326/Product: Glycoprotein VP7 #status Predicted <GPV>  
F:32-48/Region: hydrophobic fistatus predicted  
F:69,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity	Score	DB	Length
42.4%; Pred. No. 43; Mismatches 7; Conservative 4; Indels 0; Gaps 0;	42	2	326

Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SDGLWNWNNOTQFL 15  
Db 94 SDGEWKSLSQMF 107

RESULT 35

T05439

Query Match

Best Local Similarity	Score	DB	Length
42.4%; Pred. No. 43; Mismatches 7; Conservative 4; Indels 0; Gaps 0;	42	2	326

Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SDGLWNWNNOTQFL 18  
Db 303 SDPOWKGAASRIFLEHA 319

RESULT 36

AC2754

ISPD/ISPf bifunctional enzyme [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

Query Match

Best Local Similarity	Score	DB	Length
41.2%; Pred. No. 54; Mismatches 4; Conservative 7; Indels 0; Gaps 0;	42	2	400

Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SDGLWNWNNOTQFL 18  
Db 303 SDPOWKGAASRIFLEHA 319

RESULT 37

T05439

Query Match

Best Local Similarity	Score	DB	Length
42.4%; Pred. No. 54; Mismatches 4; Conservative 7; Indels 0; Gaps 0;	42	2	400

Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SDGLWNWNNOTQFL 18  
Db 303 SDPOWKGAASRIFLEHA 319

hypothetical protein F7K2-30 - *Arabidopsis thaliana* (mouse-ear cress)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T05439  
R;Bevan, M.; Wedder, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schueler, submitted to the Protein Sequence Database, November 1998  
A;Reference number: Z15416  
A;Accession: T05439  
A;Molecule type: DNA  
A;Residues: 1-457 <BSV>  
A;Cross-references: UNIPROT:Q9STX4; EMBL:AL033545  
A;Experimental source: cultivar Columbia; BAC clone F7K2  
C;Genetics:  
A;Map position: 4  
A;Introns: 8/3; 107/3; 309/3; 327/3  
A;Note: F7K2.30

Query Match

Best Local Similarity	Score	DB	Length
42.4%; Pred. No. 63; Mismatches 50.0%; Indels 0; Gaps 0;	42	2	457

Best Local Similarity 50.0%; Pred. No. 63; Mismatches 6; Indels 0; Gaps 0;

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Orellio, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Matkcz, B.; A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*  
A;Reference number: A97359; MUID:2160851; PMID:11743194  
A;Accession: A97359

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Qy 5 LWNNTQTLIE 16  
 :||: :||:  
 Db 11 WNWDTQFYLE 22

RESULT 38

A5932 cytochrome C-type biogenesis protein CCMP - Cyanidioschyzon merolae mitochondrial C;Species: mitochondrial Cyanidioschyzon merolae  
 C;Accession: A5932  
 C;Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004  
 R;Ohta, N.; Sato, T.; Kuroiwa, T.  
 Nucleic Acids Res. 26, Nucleic Acids Res. 26, 519-519, 1998  
 A;Title: Structure and organization of the mitochondrial genome of the unicellular red alga Cyanidioschyzon merolae  
 A;Reference number: A58930; MUID:99030526; PMID:9801318  
 A;Accession: A58932  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross-references: 1-620 <ARN>  
 A;Cross-references: UNIPROT:Q9ZZP7; GB:D89861; NID:94115781; PIDN:BA136527.1; PID:941157  
 C;Genetics:  
 A;Gene: yejR; ccmP  
 A;Genome: mitochondrial  
 C;Superfamily: nrnE protein  
 C;Keywords: mitochondrial

Query Match 42.4%; Score 42; DB 2; Length 620;  
 Best Local Similarity 63.6%; Pred. No. 88; Mismatches 7;  
 Matches 7; Conservative 2; Indels 2; Gaps 0; Gaps 0;  
 Matches 7; Mismatches 2; Indels 2; Gaps 0; Gaps 0;

Qy 5 LWNNTQTLIE 15  
 :||: :||:  
 Db 91 LWSNNNEGSLFL 101

RESULT 39

S75724 hypothetical protein slr0907 - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.  
 A;Variety: PCC 6803  
 C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
 C;Accession: S75724  
 R;Kaneo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O., K.; Okumura, S.; Shimpoo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.  
 A;Reference number: S74322; MUID:97061201; PMID:8905231  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-1014 <KAN>  
 A;Cross references: UNIPROT:Q55374; EMBL:D64003; GB:AB001339; NID:gi1001200; PIDN:BA1045  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 42.4%; Score 42; DB 2; Length 1014;  
 Best Local Similarity 43.8%; Pred. No. 1.5e+02; Mismatches 7;  
 Matches 7; Conservative 5; Indels 4; Gaps 0; Gaps 0;

Qy 1 SSDGLWNNTQFLIE 16  
 :||: :||:  
 Db 819 ASHGIWHTASQLFPE 834

Submitted to the EMBL Data Library, April 1996  
 A;Description: Fimbrial biogenesis genes of *Pseudomonas aeruginosa*: pilW and pilX increase the  
 homology.  
 A;Reference number: S72643  
 A;Accession: S72645  
 A;Molecule type: DNA  
 A;Residues: 1-1161 <ALM>  
 A;Cross-references: UNIPROT:Q51536; EMBL:L76605; NID:gi1246298; PIDN:AAA33502.1; PMID:91246  
 A;Experimental source: strain AOL  
 R;Ahl, R.A.; Hallinan, J.P.; Watson, A.A.; Mattick, J.S.  
 Mol. Microbiol. 22, 161-173, 1996  
 A;Title: Fimbrial biogenesis genes of *Pseudomonas aeruginosa*: pilW and pilX increase the  
 homology.  
 A;Reference number: S72631; MUID:97055431; PMID:8897918  
 A;Accession: S72633  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 657-913 <ALW>  
 A;Cross-references: EMBL:L76605  
 A;Note: only a part of the translation is shown  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1996  
 C;Genetics:  
 A;Gene: pylY  
 C;Function: may be involved in assembly of type 4 fimbriae  
 C;Keywords: fimbria; membrane protein  
 Query Match 42.4%; Score 42; DB 2; Length 1161;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 SDGLWNNTQFL 13  
 :||: :||:  
 Db 357 TDGLWNDSAV 368

Search completed: December 30, 2004, 16:13:57  
 Job time : 43 secs



OM protein - protein search, using sw model		28	29	29.3	7	2	US-08-292-968-43	Sequence 43, Appl
Run on:	December 30, 2004, 16:23:09 ; Search time 37 Seconds (without alignments)	29	29	29.3	7	2	US-08-467-974-43	Sequence 43, Appl
Copyright (c) 1993 - 2004 Compugen Ltd.		30	29	29.3	7	2	US-08-467-974-43	Sequence 43, Appl
Title:	US-10-718-321-1	31	29	29.3	7	3	US-08-467-976-43	Sequence 43, Appl
Perfect score:	99	32	29	29.3	7	3	US-08-482-514-43	Sequence 43, Appl
Sequence:	1 SSDGLWNNNRQQLFLEHHS 18	33	29	29.3	7	4	US-09-567-222C-53	Sequence 43, Appl
Scoring table:	BLOSUM62	34	29	29.3	14	4	US-09-570-921-141	Sequence 141, Appl
Gapop 10.0 , Gapext 0.5		35	29	29.3	17	4	US-10-032-330-52	Sequence 52, Appl
Searched:	478139 seqs, 66318000 residues	36	28	28.3	8	1	US-08-190-788A-19	Sequence 19, Appl
Total number of hits satisfying chosen parameters:	187706	37	28	28.3	9	1	US-08-383-474B-24	Sequence 42, Appl
Minimum DB seq length: 0		38	28	28.3	8	1	US-08-465-391A-19	Sequence 19, Appl
Maximum DB seq length: 20		39	28	28.3	8	2	US-08-465-538B-19	Sequence 60, Appl
Post-processing:	Minimum Match 0%	40	28	28.3	8	2	US-08-463-076B-63	Sequence 63, Appl
Maximum Match 100%		41	28	28.3	9	2	US-08-42B-082B-649	Sequence 64, Appl
Listing first 150 summaries		42	28	28.3	9	2	US-08-672-345C-42	Sequence 42, Appl
Database :	Issued Patents AA: *	43	28	28.3	9	3	US-08-214-095D-42	Sequence 24, Appl
1: /cgn2_6/ptodata/1/iaa/51_COMB.pep: *		44	28	28.3	11	2	US-08-42B-257A-60	Sequence 19, Appl
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *		45	28	28.3	12	1	US-08-42B-805B-84	Sequence 60, Appl
3: /cgn2_6/ptodata/1/iaa/61_COMB.pep: *		46	28	28.3	12	1	US-08-463-788A-294	Sequence 294, App
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *		47	28	28.3	12	1	US-08-42B-383-474B-295	Sequence 295, App
5: /cgn2_6/ptodata/1/iaa/potus_COMB.pep: *		48	28	28.3	12	1	US-08-465-391A-295	Sequence 295, App
6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *		49	28	28.3	12	2	US-08-466-538B-293	Sequence 293, App
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		50	28	28.3	13	3	US-08-192-048-27	Sequence 84, App
		51	28	28.3	14	2	US-08-413-708B-5	Sequence 5, Appl
		52	28	28.3	14	3	US-08-192-048-24	Sequence 24, Appl
		53	28	28.3	14	4	US-08-590-646A-23	Sequence 130, App
		54	28	28.3	15	2	US-08-592-646A-19	Sequence 19, Appl
		55	28	28.3	15	2	US-08-592-646A-20	Sequence 20, Appl
		56	28	28.3	15	2	US-08-592-646A-21	Sequence 21, Appl
		57	28	28.3	15	2	US-08-590-646A-22	Sequence 22, Appl
		58	28	28.3	15	2	US-08-590-646A-22	Sequence 23, Appl
		59	28	28.3	15	2	US-08-592-646A-23	Sequence 19, Appl
		60	28	28.3	15	3	US-08-165-422-20	Sequence 20, Appl
		61	28	28.3	15	3	US-08-165-422-21	Sequence 21, Appl
		62	28	28.3	15	3	US-08-165-422-22	Sequence 22, Appl
		63	28	28.3	15	3	US-08-165-422-22	Sequence 23, Appl
		64	28	28.3	15	3	US-08-165-422-23	Sequence 23, Appl
		65	28	28.3	15	4	US-08-157-689-73	Sequence 38, Appl
		66	28	28.3	15	5	PCT-US93-11703-39	Sequence 39, Appl
		67	28	28.3	15	5	PCT-US93-11703-39	Patent No. 5194585
		68	28	28.3	16	6	5194585-3	Patent No. 5194585
		69	28	28.3	16	6	5194585-3	Patent No. 5194585
Result	#	Score	Query	Length	DB	ID	Description	
No.								
-	-	-	-	-	-	-	-	-
1	34	34.3	19	4	US-09-441-502B-6B	Sequence 68, Appl		
2	32	32.3	12	3	US-09-187-177-2	Sequence 2, Appl		
3	32	32.3	12	5	PCT-US95-12686-2	Sequence 166, Appl		
4	32	32.3	19	1	US-08-218-025A-166.	Sequence 22, Appl		
5	31	31.3	7	1	US-08-424-957-7	Sequence 7, Appl		
6	31	31.3	7	3	US-09-035-686-7	Sequence 7, Appl		
7	31	31.3	7	3	US-09-035-686-7	Sequence 7, Appl		
8	30	30.3	13	3	US-08-502-500-6	Sequence 6, Appl		
9	30	30.3	13	3	US-08-195-006-6	Sequence 6, Appl		
10	30	30.3	13	5	PCT-US94-0764A-6	Sequence 6, Appl		
11	30	30.3	14	4	US-08-203-25	Sequence 25, Appl		
12	30	30.3	20	1	US-08-218-025A-82	Sequence 82, Appl		
13	30	30.3	20	3	US-08-612-973-73	Sequence 73, Appl		
14	30	30.3	20	3	US-08-612-973-73	Sequence 82, Appl		
15	30	30.3	20	3	US-08-927-597-73	Sequence 73, Appl		
16	30	30.3	20	3	US-08-927-597-82	Sequence 82, Appl		
17	30	30.3	20	4	US-08-635-886C-38	Sequence 25, Appl		
18	30	30.3	20	4	US-08-635-886C-47	Sequence 82, Appl		
19	30	30.3	20	4	US-08-635-886C-56	Sequence 73, Appl		
20	30	30.3	20	4	US-08-974-690C-38	Sequence 82, Appl		
21	30	30.3	20	4	US-08-974-690C-47	Sequence 47, Appl		
22	30	30.3	20	4	US-08-974-690C-56	Sequence 56, Appl		
23	30	30.3	20	4	US-08-981-710-15	Sequence 15, Appl		
24	30	30.3	20	4	US-09-881-710-17	Sequence 17, Appl		
25	30	30.3	20	4	US-08-974-685-47	Sequence 47, Appl		
26	30	30.3	20	4	US-08-974-685-56	Sequence 56, Appl		
27	30	30.3	20	4	US-08-974-685-56	Sequence 117, Appl		
28	30.3	20	4	US-08-974-690C-47				
29	30.3	20	4	US-08-974-690C-56				
30	30.3	20	4	US-08-981-710-15				
31	30	30.3	20	4	US-09-881-710-17			
32	30	30.3	20	4	US-08-974-685-47			
33	30	30.3	20	4	US-08-974-685-56			
34	30	30.3	20	4	US-08-974-690C-38			
35	30	30.3	20	4	US-08-974-690C-47			
36	30	30.3	20	4	US-08-974-690C-56			
37	30	30.3	20	4	US-08-981-710-15			
38	30	30.3	20	4	US-09-881-710-17			
39	30	30.3	20	4	US-08-974-685-47			
40	30	30.3	20	4	US-08-974-685-56			
41	30	30.3	20	4	US-08-974-685-56			
42	30	30.3	20	4	US-08-974-685-56			
43	30	30.3	20	4	US-08-974-685-56			
44	30	30.3	20	4	US-08-974-685-56			
45	30	30.3	20	4	US-08-974-685-56			
46	30	30.3	20	4	US-08-974-685-56			
47	30	30.3	20	4	US-08-974-685-56			
48	30	30.3	20	4	US-08-974-685-56			
49	30	30.3	20	4	US-08-974-685-56			
50	30	30.3	20	4	US-08-974-685-56			
51	30	30.3	20	4	US-08-974-685-56			
52	30	30.3	20	4	US-08-974-685-56			
53	30	30.3	20	4	US-08-974-685-56			
54	30	30.3	20	4	US-08-974-685-56			
55	30	30.3	20	4	US-08-974-685-56			
56	30	30.3	20	4	US-08-974-685-56			
57	30	30.3	20	4	US-08-974-685-56			
58	30	30.3	20	4	US-08-974-685-56			
59	30	30.3	20	4	US-08-974-685-56			
60	30	30.3	20	4	US-08-974-685-56			
61	30	30.3	20	4	US-08-974-685-56			
62	30	30.3	20	4	US-08-974-685-56			
63	30	30.3	20	4	US-08-974-685-56			
64	30	30.3	20	4	US-08-974-685-56			
65	30	30.3	20	4	US-08-974-685-56			
66	30	30.3	20	4	US-08-974-685-56			
67	30	30.3	20	4	US-08-974-685-56			
68	30	30.3	20	4	US-08-974-685-56			
69	30	30.3	20	4	US-08-974-685-56			
70	28	28.3	18	1	US-08-056-200-66	Sequence 66, Appl		
71	28	28.3	18	1	US-08-056-200-67	Sequence 67, Appl		
72	28	28.3	18	1	US-08-478-312-36	Sequence 36, Appl		
73	28	28.3	18	1	US-08-480-302-36	Sequence 36, Appl		
74	28	28.3	18	2	US-08-800-644-24	Sequence 24, Appl		
75	28	28.3	18	2	US-08-800-644-66	Sequence 66, Appl		
76	28	28.3	18	2	US-08-800-644-67	Sequence 67, Appl		
77	28	28.3	18	2	US-08-800-644-68	Sequence 68, Appl		
78	28	28.3	18	2	US-08-800-644-68	Sequence 68, Appl		
79	28	28.3	18	2	US-08-800-644-68	Sequence 68, Appl		
80	28	28.3	20	1	US-08-218-025A-65	Sequence 65, Appl		
81	28	28.3	20	1	US-08-107-676-18	Sequence 18, Appl		
82	28	28.3	20	3	US-08-192-048-22	Sequence 22, Appl		
83	28	28.3	20	4	US-08-298-820-18	Sequence 18, Appl		
84	28	28.3	20	5	US-08-731-357B-10	Sequence 10, Appl		
85	28	27.5	27.5	3	US-08-025-76B-242	Sequence 242, App		
86	28	27.5	27.5	4	US-08-490-070A-242	Sequence 242, App		
87	27	27.5	27.5	4	US-08-490-153-242	Sequence 242, App		
88	27	27.5	27.5	6	US-08-638-203-44	Sequence 44, Appl		
89	27	27.5	27.5	8	US-08-082-279B-1496	Sequence 1496, Ap		
90	27	27.5	27.5	8	US-08-082-279B-1496	Sequence 1496, Ap		
91	27	27.5	27.5	8	US-08-315-30B-1652	Sequence 1508, Ap		
92	27	27.5	27.5	8	US-08-083-784-1496	Sequence 1496, Ap		
93	27	27.5	27.5	8	US-08-083-784-1508	Sequence 1508, Ap		
94	27	27.5	27.5	8	US-09-350-641C-1651	Sequence 1508, Ap		
95	27	27.5	27.5	8	US-08-350-641C-1651	Sequence 1508, Ap		
96	27	27.5	27.5	8	US-08-350-641C-1651	Sequence 1508, Ap		
97	27	27.5	27.5	10	US-08-190-788A-1563	Sequence 1508, Ap		
98	27	27.5	27.5	10	US-08-383-747B-41	Sequence 1508, Ap		
99	27	27.5	27.5	10	US-08-465-391A-36	Sequence 1508, Ap		
100	27	27.5	27.5	10	US-08-465-391A-36	Sequence 1508, Ap		

101 27 27.3 10 2 US-08-679-635A-17 Sequence 17, Appl  
 102 27 27.3 10 3 US-03-419-163-17 Sequence 17, Appl  
 103 27 27.3 10 4 US-03-428-082B-667 Sequence 17, Conservativ  
 104 27 27.3 12 1 US-08-241-054-42 Sequence 42, Appl  
 105 27 27.3 12 1 US-08-390-156A-18 Sequence 18, Appl  
 106 27 27.3 12 1 US-08-439-817-22 Sequence 18, Appl  
 107 27 27.3 12 1 US-08-485-508-42 Sequence 42, Appl  
 108 27 27.3 13 1 US-08-218-025A-172 Sequence 172, App  
 109 27 27.3 15 4 US-09-514-245-124 Sequence 24, Appl  
 110 27 27.3 15 4 US-09-514-245-125 Sequence 125, App  
 111 27 27.3 15 4 US-09-514-245-150 Sequence 150, App  
 112 27 27.3 15 4 US-09-514-245-151 Sequence 151, App  
 113 27 27.3 15 5 PCT-US93-11703-36 Sequence 36, Appl  
 114 27 27.3 15 5 PCT-US93-11703-37 Sequence 37, Appl  
 115 27 27.3 16 3 US-08-847-844A-36 Sequence 36, Appl  
 116 27 27.3 17 1 US-08-218-025A-37 Sequence 153, App  
 117 27 27.3 17 2 US-08-878-546-6 Sequence 6, Appl  
 118 27 27.3 17 3 US-09-399-494-6 Sequence 6, Appl  
 119 27 27.3 17 6 5266328-11 Sequence 325, App  
 120 27 27.3 17 9 3 US-09-357-325 Sequence 56, Appl  
 121 27 27.3 19 4 US-09-082-358B-56 Sequence 37, Appl  
 122 27 27.3 19 5 US-09-847-844A-36 Sequence 37, Appl  
 123 27 27.3 20 1 US-08-218-025A-37 Sequence 11, Appl  
 124 27 27.3 20 1 US-08-614-935-11 Sequence 11, Appl  
 125 27 27.3 20 3 US-09-130-287-11 Sequence 13, Appl  
 126 26 26.3 6 4 US-08-170-769A-13 Sequence 8, Appl  
 127 26 26.3 7 1 US-08-486-721A-8 Sequence 59B, App  
 128 26 26.3 8 3 US-08-444-818-598 Sequence 7, Appl  
 129 26 26.3 9 3 US-08-727-308-7 Sequence 44, Appl  
 130 26 26.3 10 1 US-08-214-650-4 Sequence 44, Appl  
 131 26 26.3 11 2 US-08-482-228-44 Sequence 44, Appl  
 132 26 26.3 11 3 US-08-482-528-44 Sequence 44, Appl  
 133 26 26.3 12 1 US-08-190-788A-21 Sequence 21, Appl  
 134 26 26.3 12 1 US-08-241-054-38 Sequence 38, Appl  
 135 26 26.3 12 1 US-08-241-054-46 Sequence 46, Appl  
 136 26 26.3 12 1 US-08-390-156A-16 Sequence 16, Appl  
 137 26 26.3 12 1 US-08-390-156A-20 Sequence 20, Appl  
 138 26 26.3 12 1 US-08-439-817-18 Sequence 18, Appl  
 139 26 26.3 12 1 US-08-439-817-26 Sequence 26, Appl  
 140 26 26.3 12 1 US-08-383-474B-26 Sequence 38, Appl  
 141 26 26.3 12 1 US-08-485-508-38 Sequence 46, Appl  
 142 26 26.3 12 1 US-08-485-508-46 Sequence 21, Appl  
 143 26 26.3 12 1 US-08-465-391A-21 Sequence 21, Appl  
 144 26 26.3 12 2 US-08-664-538B-21 Sequence 65, Appl  
 145 26 26.3 12 2 US-08-463-076E-65 Sequence 44, Appl  
 146 26 26.3 12 4 US-09-821-823-44 Sequence 65I, Appl  
 147 26 26.3 12 4 US-09-428-082B-651 Sequence 40, Appl  
 148 26 26.3 15 5 PCT-US93-11703-40 Patent No. 5378464  
 149 26 26.3 15 6 5378464-14 Sequence 21, Appl  
 150 26 26.3 16 2 US-08-476-062A-21

## ALIGNMENTS

RESULT 1  
 US-09-441-502B-68 Application US/09441502B  
 ; Sequence 68, Application US/09441502B  
 ; Patient No. 645541  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dunbar, Bonita S.  
 ; TITLE OF INVENTION: IMMUNOGENIC EPITOPEs OF THE HUMAN ZONA PELLUCIDA PROTEIN  
 ; FILE REFERENCE: 12231.2US1  
 ; CURRENT APPLICATION NUMBER: US/09/441,502B  
 ; CURRENT FILING DATE: 1999-11-17  
 ; NUMBER OF SEQ ID NOS: 104  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 68  
 ; LENGTH: 19  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-441-502B-68

Query Match 34.3%; Score 34; DB 4; Length 19;  
 Best Local Similarity 53.8%; Pred. No. 52;  
 Matches 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSDGIGDNNTQTL 13  
 Db 1 SGSGIGDNNTQTL 13

RESULT 2  
 US-08-817-177-2 Application US/08817177  
 ; Sequence 2, Application US/08817177  
 ; Patent No. 6096314  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COHEN, Irvin R.  
 ; ADDRESS: Browd and Neimark, P.L.L.C.  
 ; STREET: 419 Seventh Street, N. W.  
 ; CITY: Washington  
 ; COUNTRY: US  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/817,177  
 ; FILING DATE:  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/12686  
 ; FILING DATE: 10-OCTOBER-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: ISRAEL APP. NO. 111,196  
 ; TELECOMMUNICATION INFORMATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROMDY, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: COHEN-27  
 ; TELEPHONE: (202) 628-5197  
 ; TELEFAX: (202) 737-3528  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SOURCE CHARACTERISTICS:  
 ; LENGTH: 12 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Peptide  
 ; US-08-817-177-2

RESULT 3  
 PCT-US95-12686-2 Application PC/TUSS9512686  
 ; Sequence 2, Application PC/TUSS9512686  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
 ; NUMBER OF SEQUENCES: 16

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
APPLICATION NUMBER: PCT/US95/12686  
FILING DATE:  
CLASSIFICATION:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-12686-2

Query Match Best Local Similarity 32.3%; Score 32; DB 5; Length 12;  
Best Local Similarity 45.5%; Pred. No. 65; Matches 5; Mismatches 5; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy	2 SDGLWNWNQDQ	1 ASSLWLNQDQ	11
Db			

RESULT 4 US-08-218-025A-166  
Patent No. 556744  
GENERAL INFORMATION:  
APPLICANT: Weiner, David B.  
APPLICANT: Ugen, Kenneth E.  
APPLICANT: Williams, William V.  
TITLE OF INVENTION: Methods and Compositions for Diagnosing  
TITLE OF INVENTION: and Treating Certain HIV Infected Patients  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: P.O. Box 457, 321 No. 555674 Aristown Road  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19477

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
REFERENCE/DOCKET NUMBER: A-60244/WHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 27299

INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

US-08-277-660A-22

Query Match Best Local Similarity 31.3%; Score 31; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 5; Mismatches 0; Indels 0; Gaps 0;

Qy	2 SDGLW 6	3 SDGLW 7
Db		

RESULT 6 US-08-424-957-7  
Sequence 7, Application US/08424957  
Patent No. 5770377  
GENERAL INFORMATION:  
APPLICANT: Picklesley, Steven M.  
APPLICANT: Lane, David P.  
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flent, Rohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco

INFORMATION FOR SEQ ID NO: 166:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-218-025A-166

Query Match 32.3%; Score 32; DB 1; Length 19;

STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,957  
 FILING DATE: 19-APR-1995  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994

ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190

REFERENCE DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEX: 910 277299

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown

US-08-424-957-7

Query Match 31.3%; Score 31; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2 SDGLW 6
Db	3 SDGLW 7

RESULT 8

US-08-592-500-6

Query Match 31.3%; Score 31; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2 SDGLW 6
Db	3 SDGLW 7

RESULT 8

US-08-592-500-6

Sequence 6, Application US/08592500  
 Patent No. 60508

GENERAL INFORMATION:  
 APPLICANT: Lanza, Francois  
 APPLICANT: Phillips, David R.  
 APPLICANT: Cazenave, Jean-Pierre  
 TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend Khourie and Crew  
 STREET: 379 Lurton Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: US  
 ZIP: 94301

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/592,500  
 FILING DATE:  
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/089,455  
 FILING DATE: 09-JUL-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Dow, Karen B.

REGISTRATION NUMBER: 29,684  
 REFERENCE DOCKET NUMBER: 12418-28  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 326-2400  
 TELEX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide

FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..13  
 OTHER INFORMATION: /note= "K5/6 peptide residues  
 OTHER INFORMATION: 1-13."

US-08-592-500-6

Query Match 30.3%; Score 30; DB 3; Length 13;

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/424,957  
 FILING DATE: 19-APR-1995  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994

ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.

Best Local Similarity 71.4%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
 US-08-195-006-6 Application US/08195006  
 ; Sequence 6, Application PC/TUS9407644A  
 ; GENERAL INFORMATION:  
 ; PATENT NO. 6081688  
 ; Db 7 QLFLEHNS 13

GENERAL INFORMATION:  
 APPLICANT: Lanza, Francois  
 APPLICANT: Phillips, David R.  
 APPLICANT: Cazenave, Jean-Pierre  
 TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses  
 NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend Khourie and Crew  
 STREET: 379 Lytton Avenue  
 CITY: Palo Alto  
 STATE: California  
 ZIP: 94301

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 OPERATING SYSTEM: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/195, 006  
 FILING DATE: 10-FEB-1994  
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/089, 455  
 FILING DATE: 09-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dow, Karen B.  
 REGISTRATION NUMBER: 29, 684  
 REFERENCE/DOCKET NUMBER: 12418-28

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 325-2400  
 TELEFAX: (415) 326-4222

SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..13  
 OTHER INFORMATION: /note= "K5/6 peptide residues  
 OTHER INFORMATION: 1-13."

Query Match  
 Best Local Similarity 71.4%; Pred. No. 1.5e+02; Length 13;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 PCT-US94-07644A-6

RESULT 11  
 US-09-638-203-25  
 ; Sequence 25, Application US/09638203  
 ; Patent No. 660201  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Aya Jakobovits  
 ; APPLICANT: Arthur B. Rattano  
 ; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE  
 ; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF  
 ; FILE REFERENCE: 129\_20US01  
 ; CURRENT APPLICATION NUMBER: US/09/638, 203  
 ; CURRENT FILING DATE: 2000-08-11  
 ; PRIOR APPLICATION NUMBER: 60/148, 935  
 ; PRIOR FILING DATE: 1999-08-12  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 25  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; US-09-638-203-25

Query Match  
 Best Local Similarity 55.6%; Pred. No. 1.6e+02; Length 14;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 APPLICANT: COR Therapeutics, Inc.  
 TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses  
 NUMBER OF SEQUENCES: 43

RESULT 10  
 PCT-US94-07644A-6  
 ; Sequence 6, Application PC/TUS9407644A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COR Therapeutics, Inc.  
 ; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses  
 ; NUMBER OF SEQUENCES: 43

Query Match  
 Best Local Similarity 30.3%; Score 30; DB 4; Length 14;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 APPLICANT: COR Therapeutics, Inc.  
 TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses  
 NUMBER OF SEQUENCES: 43

Db            1 GLWRNGDQQ 9

RESULT 12  
US-08-218-025A-82  
Sequence 82, Application US/08218025A  
Patent No. 5556744  
GENERAL INFORMATION:  
APPLICANT: Weiner, David B.  
APPLICANT: Ugen, Kenneth E.  
APPLICANT: Williams, William V.  
TITLE OF INVENTION: Methods and Compositions for Diagnosing  
TITLE OF INVENTION: and Treating Certain HIV Infected Patients  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howton and Howton  
STREET: P.O. Box 457, 321 NO. 5556744ristown Road  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19477

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patient In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,973  
FILING DATE: 11-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide

US-08-612-973-73

REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST33A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9206  
TELEFAX: (215) 540-5818

INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-218-025A-82

Query Match            30.3%; Score 30; DB 1; Length 20;  
Best Local Similarity            38.5%; Pred. No. 2.4e+02; Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY            3 DGLWNW 8  
Db            1 DDIWN 6

RESULT 13  
US-08-612-973-73  
Sequence 73, Application US/08612973  
Patent No. 6150134  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT  
APPLICANT: BOSMAN, FONS  
APPLICANT: DE MARTYNOFF, GUY  
APPLICANT: BUYSE, MARIE-ANGE  
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE  
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYPE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patient In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,973  
FILING DATE: 11-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-612-973-82

Query Match 30.3%; Score 30; DB 3; Length 20;  
Best Local Similarity 40.0%; Pred. No. 2.4e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNOTQFL 15  
Db 7 WGENDTDVFV 16

RESULT 15

US-08-927-597-73

Sequence 73, Application US/08927597

Patent No. 6245503

GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT

BOSMAN, FONS

DE MARTYNOFF, GUY

BUYSE, MARIE-ANGE

APPLICANT: MAERTENS, GERT

BOSMAN, FONS

DE MARTYNOFF, GUY

BUYSE, MARIE-ANGE

APPLICANT: BUYSE, MARIE-ANGE

PURIFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF INVENTION: 111

NUMBER OF SEQUENCES: 111

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHVE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-927-597-73

Query Match 30.3%; Score 30; DB 3; Length 20;  
Best Local Similarity 38.5%; Pred. No. 2.4e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SDGGLWNNNOTQFL 13  
Db 7 NTNGQWHMNSTL 19

RESULT 16

US-08-927-597-82

Sequence 82, Application US/08927597

Patent No. 6245503

GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT

BOSMAN, FONS

DE MARTYNOFF, GUY

BUYSE, MARIE-ANGE

APPLICANT: BUYSE, MARIE-ANGE

PURIFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

RESULT 17

US-08-635-886C-38

Sequence 38, Application US/08635886C

Patent No. 6555114

GENERAL INFORMATION:

APPLICANT: LEROUX-ROBLIS, Geert

APPLICANT: DELBYS, Robert

APPLICANT: MAERTENS, Geert

TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

FILE REFERENCE: 2752-18

CURRENT APPLICATION NUMBER: US/08/635, 886C

PRIOR APPLICATION NUMBER: PCT/EP94/03555

PRIOR FILING DATE: 1994-10-28

PRIOR APPLICATION NUMBER: EP 93402718.6

```

; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-38

Query Match 30.3%; Score 30; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.4e+02; Matches 4; Conservat 2; Mismatches 4; Indels 0; Gaps 0;
Qy 6 WNNNOTQFL 15
Db 7 WGENDTDVFL 16

RESULT 18
US-08-635-886C-47
; Sequence 47, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELIS, Geert
; APPLICANT: DELBYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-47

Query Match 30.3%; Score 30; DB 4; Length 20;
Best Local Similarity 38.5%; Pred. No. 2.4e+02; Matches 5; Conservat 4; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SSDGWMNNNOTL 13
Db 7 NTNGSWHINSTAL 19

RESULT 19
US-08-635-886C-56
; Sequence 56, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELIS, Geert
; APPLICANT: DELBYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-56

Query Match 30.3%; Score 30; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.4e+02; Matches 4; Conservat 2; Mismatches 4; Indels 0; Gaps 0;
Qy 6 WNNNOTQFL 15
Db 7 WGENDTDVFL 16

```

```

RESULT 21
; US-08-974-690C-47
; Sequence 47, Application US/08974690C
; Patent No. 6513333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MARTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPESES OF HEPATITIS C VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
; US-08-974-690C-47

RESULT 22
; Query Match 30.3%; Score 30; DB 4; Length 20;
; Best Local Similarity 38.5%; Pred. No. 2.4e+02; Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0; Other Information: Xaa is Thr or Ser
; Sequence 56, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MARTENS, Geert
; APPLICANT: JEROUDT-RIBOLIS, Geert
; APPLICANT: DELBEK, Vincent
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPESES OF HEPATITIS C VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
; US-08-974-690C-47

RESULT 23
; Query Match 30.3%; Score 30; DB 4; Length 20;
; Best Local Similarity 38.5%; Pred. No. 2.4e+02; Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0; Other Information: Xaa is Ser or Arg
; Sequence 15, Application US/09881710
; Patent No. 667395
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: COURAGE, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671US0
; CURRENT APPLICATION NUMBER: US/09/881,710
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dengue virus
; US-09-881-710-15

RESULT 24
; Query Match 30.3%; Score 30; DB 4; Length 20;
; Best Local Similarity 50.0%; Pred. No. 2.4e+02; Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0; Other Information: Xaa is Leu or Ile
; Sequence 17, Application US/09881710
; Patent No. 667395
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: COURAGE, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671US0
; CURRENT APPLICATION NUMBER: US/09/881,710
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
; US-09-881-710-15

RESULT 25
; Query Match 30.3%; Score 30; DB 4; Length 20;
; Best Local Similarity 50.0%; Pred. No. 2.4e+02; Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0; Other Information: Xaa is Leu or Ile
; Sequence 19, Application US/09881710
; Patent No. 667395
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: COURAGE, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671US0
; CURRENT APPLICATION NUMBER: US/09/881,710
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
; US-09-881-710-15

RESULT 26
; Query Match 30.3%; Score 30; DB 4; Length 20;
; Best Local Similarity 50.0%; Pred. No. 2.4e+02; Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0; Other Information: Xaa is Leu or Ile
; Sequence 19, Application US/09881710
; Patent No. 667395
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: COURAGE, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671US0
; CURRENT APPLICATION NUMBER: US/09/881,710
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
; US-09-881-710-15

RESULT 27
; Query Match 30.3%; Score 30; DB 4; Length 20;
; Best Local Similarity 50.0%; Pred. No. 2.4e+02; Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0; Other Information: Xaa is Leu or Ile
; Sequence 19, Application US/09881710
; Patent No. 667395
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: COURAGE, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671US0
; CURRENT APPLICATION NUMBER: US/09/881,710
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
; US-09-881-710-15

```

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Dengue virus  
; US-09-801-710-17;

Query Match 30.3%; Score 30; DB 4; Length 20;  
Best Local Similarity 38.5%; Pred. No. 2.4e+02; Mismatches 5; Conservative 5; Matches 5; Indels 0; Gaps 0;

Qy 1 SDGGLWNNNQ 10  
Db 10 SSEGAWKHAQ 19

RESULT 25  
US-08-974-685-47  
Sequence 47, Application US/08974685  
Patent No. 6689368  
GENERAL INFORMATION:  
APPLICANT: LEROUIX-ROELS, GEERT  
DELEYS, ROBERT  
MARTENS, GEERT  
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND THERAPEUTIC COMPOSITIONS CONTAINING THE SAME  
NUMBER OF SEQUENCES: 181  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,685  
FILING DATE: 19-No. 6689368-1997  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1407-11  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLogy: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 2  
OTHER INFORMATION: Xaa is Asn or Lys or Asp or Arg  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 3  
OTHER INFORMATION: Xaa is Val or Ile or Leu  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 4  
OTHER INFORMATION: Xaa is Gln or Ser or Tyr  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 6  
OTHER INFORMATION: Xaa is Ile or Val  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 8  
OTHER INFORMATION: Xaa is Thr or Ser  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 14  
OTHER INFORMATION: Xaa is Ieu or Ile  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 16  
OTHER INFORMATION: Xaa is Ser or Arg  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-08-974-685-56

Query Match 30.3%; Score 30; DB 4; Length 20;  
Best Local Similarity 38.5%; Pred. No. 2.4e+02; Mismatches 5; Conservative 5; Matches 5; Indels 0; Gaps 0;

Qy 1 SDGGLWNNNQ 13  
Db 7 NTNGSWHINSTL 19

RESULT 26  
US-08-974-685-56  
Sequence 56, Application US/08974685

Qy 1 SSDGLWNNOTQL 13  
 : : | : |  
 Db 7 NXNGSWHXXNXTAL 19

RESULT 27  
 US-08-014-979-117  
 Sequence 117, Application US/08014979

PATENT NO. 5510240

GENERAL INFORMATION:  
 TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of Use Thereof

NUMBER OF SEQUENCES: 121  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/014,979  
 FILING DATE: 19930208  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mirock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 7156-041

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 790-9080  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 MOLECULE TYPE: peptide

US-08-014-979-117

Query Match 29,3%; Score 29; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WNNN 9  
 Db 1 WNNN 4

RESULT 28  
 US-08-292-968-43  
 Sequence 43, Application US/08292968

PATENT NO. 5656122

GENERAL INFORMATION:  
 APPLICANT: READ, Randy J.

APPLICANT: STEIN, Penelope E.

APPLICANT: COCKLE, Stephen A.

APPLICANT: OOMEN, Raymond P.

APPLICANT: LOOSMORE, Sheena

APPLICANT: KUBIN, Michel H.

APPLICANT: ARMSTRONG, Glen D.

APPLICANT: HAZES, Bart

TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN

NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: MSG 1R7

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/292,968

FILING DATE:  
 FILING DATE: 24-AUG-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/110,947

PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/251,121

ATTORNEY/AGENT INFORMATION:  
 NAME: STEWART, Michael I.

REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-388  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US-08-292-968-43

Query Match 29,3%; Score 29; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DGLWN 8  
 Db 2 NGLWN 7

RESULT 29  
 US-08-467-974-43  
 Sequence 43, Application US/08467974

PATENT NO. 5965385

GENERAL INFORMATION:

APPLICANT: READ, Randy J.

APPLICANT: STEIN, Penelope E.

APPLICANT: COCKLE, Stephen A.

APPLICANT: OOMEN, Raymond P.

APPLICANT: LOOSMORE, Sheena

APPLICANT: KUBIN, Michel H.

APPLICANT: ARMSTRONG, Glen D.

APPLICANT: HAZES, Bart

TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN

NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue

CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: MSG 1R7

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,974

APPLICATION NUMBER: US/08/467,974  
 FILING DATE: 31-MAY-1994  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/467,536  
 FILING DATE: 06-JUN-1995  
 APPLICATION NUMBER: US 08/292,968  
 FILING DATE: 22-AUG-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/251,121  
 FILING DATE: 31-MAY-1994  
 APPLICATION NUMBER: US 08/110,947  
 FILING DATE: 24-AUG-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEWART, Michael I.  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-455 MIS:vg  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/110,947  
 FILING DATE: 24-AUG-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEWART, Michael I.  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-454 MIS:vg  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 FAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-467-974-43

Query Match 29.3%; Score 29; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DGLMNN 8  
 Db 2 NGLWNND 7

RESULT 30  
 US-08-467-536-43  
 Sequence 43, Application US/08467536  
 Patent No. 6018022  
 GENERAL INFORMATION:  
 APPLICANT: READ, Randy J.  
 APPLICANT: STEIN, Penelope E.  
 APPLICANT: COCKLE, Stephen A.  
 APPLICANT: OOMEN, Raymond P.  
 APPLICANT: LOOSMORE, Sheena  
 APPLICANT: KLEIN, Michel H.  
 APPLICANT: ARMSTRONG, Glen D.  
 APPLICANT: HAZES, Bart  
 APPLICANT: ARMSTRONG, Glen D.  
 APPLICANT: HAZES, Bart  
 TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN  
 NUMBER OF SEQUENCES: 45  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: MSG 1R7

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,976  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/292,968  
 FILING DATE: 22-AUG-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/251,121  
 FILING DATE: 31-MAY-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/110,947  
 FILING DATE: 24-AUG-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEWART, Michael I.  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-453 MIS:vg

US-08-467-974-43

RESULT 31  
 US-08-467-976-43  
 Sequence 43, Application US/08467976  
 Patent No. 6018022  
 GENERAL INFORMATION:  
 APPLICANT: READ, Randy J.  
 APPLICANT: STEIN, Penelope E.  
 APPLICANT: COCKLE, Stephen A.  
 APPLICANT: OOMEN, Raymond P.  
 APPLICANT: LOOSMORE, Sheena  
 APPLICANT: KLEIN, Michel H.  
 APPLICANT: ARMSTRONG, Glen D.  
 APPLICANT: HAZES, Bart  
 APPLICANT: ARMSTRONG, Glen D.  
 APPLICANT: HAZES, Bart  
 TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: MSG 1R7

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,976  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/292,968  
 FILING DATE: 22-AUG-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/251,121  
 FILING DATE: 31-MAY-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/110,947  
 FILING DATE: 24-AUG-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEWART, Michael I.  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-453 MIS:vg

US-08-467-976-43

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

US-08-467-976-43

Query Match 29.3%; Score 29; DB 3; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DGLWNN 8 Db 2 NGLWND 7

RESULT 32  
 US-09-082-514-43  
 Sequence 43, Application US/09082514

GENERAL INFORMATION:

APPLICANT: READ, Randy J.

APPLICANT: STEIN, Penelope E.

APPLICANT: COCKLE, Stephen A.

APPLICANT: OONEN, Raymond P.

APPLICANT: KLEIN, Michael H.

APPLICANT: ARMSTRONG, Glen D.

APPLICANT: HAZES, Bart

TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: SIM &amp; McBURNEY

STREET: 6th Floor, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: MSG 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patient Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/082,514

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/292,968

FILING DATE: 24-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: STEWART, Michael I.

REGISTRATION NUMBER: 24,973

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

US-09-082-514-43

Query Match 29.3%; Score 29; DB 4; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 QTOQLEH 17 Db 1 KTOQLEH 8

RESULT 33  
 US-09-563-222C-53  
 Sequence 53, Application US/09563222C

GENERAL INFORMATION:

APPLICANT: HEIN, MICH B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6966620

CURRENT APPLICATION NUMBER: US/09/563,222C

CURRENT FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: PCT/US01/14349

PRIOR FILING DATE: 2001-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 34  
 US-09-570-921-141  
 Sequence 141, Application US/09570921

GENERAL INFORMATION:

APPLICANT: SERRES, PIERRE-FRANCOIS

TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE PATHOGENIC EFFECTS RELATED TO A RETROVIRAL INFECTION

FILE REFERENCE: 106213

CURRENT APPLICATION NUMBER: US/09/570,921

CURRENT FILING DATE: 2000-05-15

PRIOR APPLICATION NUMBER: PCT/FR98/02447

PRIOR FILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: FR/97/14387

PRIOR FILING DATE: 1997-11-17

NUMBER OF SEQ ID NO: 144

SOFTWARE: PatientIn Ver. 2.1

SEQ ID NO: 141

LENGTH: 14

TYPE: PRT

ORGANISM: Human

RESULT 35  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: EPICITE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 36  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: HEIN, MICH B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 37  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: EPICITE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 38  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: HEIN, MICH B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 39  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: EPICITE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 40  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: HEIN, MICH B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 41  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: EPICITE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 42  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: HEIN, MICH B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 43  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: EPICITE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 44  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: HEIN, MICH B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 45  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: EPICITE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 46  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: HEIN, MICH B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 47  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: EPICITE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 48  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: HEIN, MICH B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 49  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: EPICITE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 50  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: HEIN, MICH B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT APPLICATION NUMBER: PCT/US01/14349

CURRENT FILING DATE: 2000-05-02

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 53

RESULT 51  
 US-10-032-330-52  
 Sequence 52, Application US/10032330

GENERAL INFORMATION:

APPLICANT: EPICITE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

PATENT NO.: 6770626

CURRENT

; GENERAL INFORMATION:  
; APPLICANT: Ben-Sasson, Shmuel  
; TITLE OF INVENTION: Tissue Remodeling  
; FILE REFERENCE: BEN-SASSON=7  
; CURRENT APPLICATION NUMBER: US/11/032,330  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: PCT/US00/32852  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: US 09/161,094  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; US-10-032-330-52

Query Match 29.3%; Score 29; DB 4; Length 17;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
Db 1 SDGGLNNQGQFL 15  
Db 1 SDMTSRNSSTQDWL 14

RESULT 36  
US-08-190-788A-19  
Sequence 19 Application US/08190788A  
Patent No. 5608035  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Stephen D.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Baldwin, David N.  
APPLICANT: Jacobs, Jeff W.  
TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-1 Receptor  
TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-1 Receptor  
NUMBER OF SEQUENCES: 312  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend & Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/383,474B  
FILING DATE: 01-FEB-1995  
CLASSIFICATION: 530  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/190,788  
FILING DATE: 02-FEB-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36 691  
REFERENCE/DOCKET NUMBER: 1019.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-383-474B-24

Query Match 28.3%; Score 28; DB 1; Length 8;  
Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Db 1 SSDGILW 6  
Db 3 TDGGLW 8

RESULT 38  
US-08-465-391A-19  
Sequence 19 Application US/08465391A  
Patent No. 5786331

INFO FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

**GENERAL INFORMATION:**

APPLICANT: Barrett, Ronald W.  
 APPLICANT: Yanofsky, Stephen D.  
 GENERAL INFORMATION:  
 APPLICANT: Baldwin, David  
 APPLICANT: Jacobs, Jeff W.  
 APPLICANT: Bovy, Phillip R.  
 APPLICANT: Leahy, Ellen M.  
 APPLICANT: Potoff, Richard S.  
 TITLE OF INVENTION: Peptides and Compounds That Bind to the  
 NUMBER OF SEQUENCES: 405  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: USA  
 ZIP: 94105  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
**CURRENT APPLICATION DATA:**  
 APPLICATION NUMBER: US/08/465,391A  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/373,474  
 FILING DATE: 02-FEB-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 5706331viel, Vern  
 REGISTRATION NUMBER: 32,483  
 REFERENCE/DOCKET NUMBER: 16528A-001840/1019 2A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-326-2400  
 TELEFAX: 415-326-2422  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-464-538B-19  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-464-538B-19  
 RESULT 40  
 Query Match 28.3%; Score 28; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Sequence 19, Application US/08464538B  
 General Information:  
 APPLICANT: Barrett, Ronald W.  
 APPLICANT: Yanofsky, Stephen D.  
 TITLE OF INVENTION: Peptides and Compounds That Bind to the  
 NUMBER OF SEQUENCES: 392  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463, 076E  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Snyder, Joseph R.  
REGISTRATION NUMBER: 39, 381  
REFERENCE/DOCKET NUMBER: 16528A-001850US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-463-0763-63

Query Match 28.3%; Score 28; DB 2; length 8;  
Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SSDGLW 6  
DB 3 TDDGLW 8

Search completed: December 30, 2004, 16:32:49  
Job time : 39 secs

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6  
December 30, 2004, 16:31:35 ; Search time 141 Seconds

### OM protein - protein search, using sw model

Run on:

December 30, 2004, 16:31:35 ; (without alignments)  
45.923 Million cell updates/sec

Title: US-10-718-321-1  
Perfect score: 99  
Sequence: 1 SSDGLWNANNQTOFLFLEHS 18  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters:  
Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : Published Applications AA:\*

1: /cggn2\_6/prodata/1/pubpaal/US07\_PUBCOMB.pep:\*

2: /cggn2\_6/prodata/1/pubpaal/PCT\_NEW\_PUB.pep:\*

3: /cggn2\_6/prodata/1/pubpaal/US05\_NEW\_PUB.pep:\*

4: /cggn2\_6/prodata/1/pubpaal/US06\_PUBCOMB.pep:\*

5: /cggn2\_6/prodata/1/pubpaal/US07\_NEW\_PUB.pep:\*

6: /cggn2\_6/prodata/1/pubpaal/PCTIS\_PUBCOMB.pep:\*

7: /cggn2\_6/prodata/1/pubpaal/US08\_NEW\_PUB.pep:\*

8: /cggn2\_6/prodata/1/pubpaal/US08\_PUBCOMB.pep:\*

9: /cggn2\_6/prodata/1/pubpaal/US09\_PUBCOMB.pep:\*

10: /cggn2\_6/prodata/1/pubpaal/US09\_PUBCOMB.pep:\*

11: /cggn2\_6/prodata/1/pubpaal/US09C\_PUBCOMB.pep:\*

12: /cggn2\_6/prodata/1/pubpaal/US09\_NNEW\_PUB.pep:\*

13: /cggn2\_6/prodata/1/pubpaal/US0A\_PUBCOMB.pep:\*

14: /cggn2\_6/prodata/1/pubpaal/US0B\_PUBCOMB.pep:\*

15: /cggn2\_6/prodata/1/pubpaal/US0C\_PUBCOMB.pep:\*

16: /cggn2\_6/prodata/1/pubpaal/US0D\_PUBCOMB.pep:\*

17: /cggn2\_6/prodata/1/pubpaal/US10\_NNEW\_PUB.pep:\*

18: /cggn2\_6/prodata/1/pubpaal/US11\_NNEW\_PUB.pep:\*

19: /cggn2\_6/prodata/1/pubpaal/US60\_NNEW\_PUB.pep:\*

20: /cggn2\_6/prodata/1/pubpaal/US60\_PUBCOMB.pep:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34.3	12	16 US-10-649-873-131	Sequence 131, App
2	34.3	20	14 US-10-225-567A-1690	Sequence 1690, App
3	33.3	18	14 US-10-418-201-18	Sequence 18, App
4	33.3	20	10 US-09-974-879-288	Sequence 288, App
5	33.3	20	10 US-09-305-736-276	Sequence 276, App
6	33.3	20	10 US-09-818-683-276	Sequence 276, App
7	33.3	20	11 US-09-818-683-276	Sequence 276, App
8	33.3	20	15 US-10-621-401-288	Sequence 288, App
9	33.3	19	14 US-10-102-143-28	Sequence 28, App
10	31.3	20	14 US-10-029-386-31498	Sequence 31498, App
11	30.3	12	11 US-09-805-290A-15	Sequence 15, App
12	30.3	13	14 US-10-212-499-6	Sequence 6, App
13	30.3	14	10 US-09-932-613-254	Sequence 254, App

RESULT 1  
US-10-640-873-131  
; Sequence 131, Application US/10649873  
; Publication No. US20040171552A1

---

GENERAL INFORMATION:  
APPLICANT: Biokine Therapeutics Ltd.  
SEQUENCE APPLICANT: Peled, Amnon  
SEQUENCE APPLICANT: Elzengberg, Orly  
SEQUENCE APPLICANT: Vatzel-Ohayon, Dalit  
TITLE OF INVENTION: NOVEL CHMOKINE BINDING PEPTIDES CAPABLE OF MODULATING THE  
FILE REFERENCE: 26732  
CURRENT APPLICATION NUMBER: US/10/649,873  
CURRENT FILING DATE: 2003-05-28  
NUMBER OF SEQ ID NOS: 157  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 131  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide

US-10-649-873-131

Query Match Score 34; DB 16; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 6 WNNWQTO 12  
Db ||:|||  
2 WNSNNTQ 8

RESULT 2  
US-10-225-567A-1690

Sequence 1690, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
SEQUENCE APPLICANT: LifeSpan Biosciences  
SEQUENCE APPLICANT: Brown, Joseph P.  
SEQUENCE APPLICANT: Burner, Gleena C.  
SEQUENCE APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 190-04-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIORITY APPLICATION NUMBER: 60/1257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1690  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-225-567A-1690

Query Match Score 34.3%; DB 14;  
Best Local Similarity 66.7%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SSDGLWNNN 9  
Db ||:|||  
12 SSSDWNN 20

RESULT 3  
US-10-418-820-18

SEQUENCE APPLICANT: Wilson, C. Ron  
TITLE OF INVENTION: ANTIODIES FOR ENZYMES OF THE W-OXIDATION PATHWAY AND METHODS  
FILE REFERENCE: US/10/418,820  
CURRENT APPLICATION NUMBER: US/10/418,820  
CURRENT FILING DATE: 2003-04-18

---

ALIGNMENTS



; FILE REFERENCE: PZ020P1  
; CURRENT APPLICATION NUMBER: US/09/818,683  
; CURRENT FILING DATE: 2001-03-28  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO: 276  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-818-683-276  
; Query Match 33.3%; Score 33; DB 10; Length 20;  
; Best Local Similarity 50.0%; Pred. No. 3.3e+02; 5; Indels 0; Gaps 0;  
; Matches 7; Conservative 2; Mismatches 5;  
; Qy 5 LWNNTQTLFHS 18  
; Db 5 LVTNNQTQLQEA 18  
; RESULT 7  
; US-09-818-683-276  
; Sequence 276, Application US/09818683  
; Publication No. US20040165440A9  
; GENERAL INFORMATION:  
; APPLICANT: Feng et al.  
; TITLE OF INVENTION: 125 Human Secreted Proteins  
; FILE REFERENCE: PZ020P1  
; CURRENT APPLICATION NUMBER: US/09/818,683  
; CURRENT FILING DATE: 2001-03-18  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 612  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 276  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-818-683-276  
; Query Match 33.3%; Score 33; DB 11; Length 20;  
; Best Local Similarity 50.0%; Pred. No. 3.3e+02; 5; Indels 0; Gaps 0;  
; Matches 7; Conservative 2; Mismatches 5;  
; Qy 5 LWNNTQTLFHS 18  
; Db 5 LVTNNQTQLQEA 18  
; RESULT 8  
; US-10-621-401-288  
; Query Match 33.3%; Score 33; DB 11; Length 20;  
; Best Local Similarity 50.0%; Pred. No. 3.3e+02; 5; Indels 0; Gaps 0;  
; Matches 7; Conservative 2; Mismatches 5;  
; Qy 5 LWNNTQTLFHS 18  
; Db 5 LVTNNQTQLQEA 18  
; RESULT 9  
; US-10-102-143-28  
; Sequence 28, Application US/10102143  
; Publication No. US20030185851A1  
; GENERAL INFORMATION:  
; APPLICANT: Soldati, Dominique  
; APPLICANT: Meissner, Markus  
; TITLE OF INVENTION: TET transactivator system  
; FILE REFERENCE: 04630/016001  
; CURRENT APPLICATION NUMBER: US/10/102,143  
; CURRENT FILING DATE: 2003-01-21  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: TATI-3  
; OTHER INFORMATION: presumed amino acid sequence of activating domain  
; US-10-102-143-28  
; Query Match 31.3%; Score 31; DB 14; Length 19;  
; Best Local Similarity 60.0%; Pred. No. 6.5e+02; 6; Indels 0; Gaps 0;  
; Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
; Qy 6 WNNNTQQLFL 15  
; Db 8 WNNTQPYLGL 17  
; RESULT 10  
; US-10-029-386-31498  
; Sequence 31498, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GR  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 31498  
; LENGTH: 20  
; TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC020728.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.99

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5

Query Match

Score 31; DB 14; Length 20;

Best Local Similarity 60.0%; Pred. No. 6.9e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 NNNNQTQFLFLE 16  
Db 6 NYNNQNQNLME 15

RESULT 11

US-09-805-290A-15

; Sequence 15, Application US/09805290A

; Publication No. US20040002583A1

GENERAL INFORMATION:

; APPLICANT: BEZEMER, Sandra

; APPLICANT: VAN DER BURG, Monique

; APPLICANT: DE HAARD, Johannes J

; APPLICANT: TARSIUS, Erwin

TITLE OF INVENTION: USE OF ANTIBODIES

FILE REFERENCE: F7526-US [V1; PEK/JVTI seq11829Aug2001

CURRENT APPLICATION NUMBER: US/09/805,290A

PRIORITY APPLICATION NUMBER: EP 00200930.6

PRIOR FILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS.: 34

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO. 15

LENGTH: 12

TYPE: PRT

ORGANISM: lama sp.

US-09-805-290A-15

Query Match 30.3%; Score 30; DB 11; Length 12;

Best Local Similarity 62.5%; Pred. No. 5.8e+02; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSDGLWNN 8  
Db 4 SYDGSWND 11

RESULT 12

US-09-212-499-6

; Sequence 6, Application US/10212499

; Publication No. US20030135036A1

GENERAL INFORMATION:

; APPLICANT: Lanza, Francois

; APPLICANT: Phillips, David R.

; APPLICANT: Cazenave, Jean-Pierre

TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morgan Lewis &amp; Bockius LLP

STREET: 1800 M St., NW

CITY: Washington

STATE: DC

COUNTRY: US

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/212,499

FILING DATE: 06-Aug-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/560,814

FILING DATE: 2000-04-28

APPLICATION NUMBER: US 08/089,455

FILING DATE: 1993-07-09

APPLICATION NUMBER: US 08/195,006

FILING DATE: 1994-02-10

APPLICATION NUMBER: US 08/884,571

FILING DATE: 1997-06-27

ATTORNEY/AGENT INFORMATION:

NAME: Reid G. Adler

REGISTRATION NUMBER: 30,988

REFERENCE/DOCKET NUMBER: 44481-5018-04-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-467-7000

TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

MOLECULE TYPE: peptide

FEATURE: NAME/KEY: Peptide

LOCATION: 1..13

OTHER INFORMATION: /note= "KS/6 peptide residues 1-13"

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-212-499-6

Query Match 30.3%; Score 30; DB 14; Length 13;

Best Local Similarity 71.4%; Pred. No. 6.3e+02; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QLFLEHS 18  
Db 7 QLFQDH 13

RESULT 13

US-09-932-613-254

; Sequence 254, Application US/09932613

; Publication No. US20030091565A1

GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; APPLICANT: Beltzner, James P.

; APPLICANT: Potter, M. Daniel

; APPLICANT: Rosen, Craig A.

; APPLICANT: Fleming, Tony J.

; APPLICANT: Cazenave, Jean-Pierre

TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON

FILE REFERENCE: DYX-025.1.PCT; DYX-025.1.US

CURRENT APPLICATION NUMBER: US/09/932,613

CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS.: 45B

SOFTWARE: PatentIn version 3.1

SEQ ID NO. 254

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: BLYS binding polypeptide

US-09-932-613-254

Query Match 30.3%; Score 30; DB 10; Length 14;

Best Local Similarity 38.5%; Pred. No. 6.8e+02; Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LWNNTQTFLEH 17  
Db 2 IWDPLTKLWLPH 14

RESULT 14  
US-09-932-322-254  
; Sequence 254, Application US/09932322  
; Publication No. US20030194743A1  
; GENERAL INFORMATION:  
; APPLICANT: Dyax Corp.  
; APPLICANT: Beltzner, James P.  
; APPLICANT: Porter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Ladner, Robert Charles  
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLYS)  
; FILE REFERENCE: DDX-018.1 PCT; DDX-018.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,322  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 254  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: BLYS binding polypeptide  
US-09-932-322-254  
Query Match 30.3%; Score 30; DB 10; Length 14;  
Best Local Similarity 38.5%; Pred. No. 6.8e+02;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
Qy 5 WNNNNOTQFLEH 17  
Db 2 IWDPLTKUWLPH 14

RESULT 15  
US-10-460-512-25  
; Sequence 25, Application US/10460512  
; Publication No. US20040038271A1  
; GENERAL INFORMATION:  
; APPLICANT: Daniel E. H. Afar  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Aya Jakobovits  
; APPLICANT: Arthur B. Raitano  
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF  
; TITLE OF INVENTION: ANTI-GEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/10/460,512  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: US/09/638,203  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/148,935  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 25  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-460-512-25

Query Match 30.3%; Score 30; DB 15; Length 14;  
Best Local Similarity 55.6%; Pred. No. 6.8e+02; Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GLMWNNOQ 12  
Db 1 GLWRNGDQQ 9

RESULT 16  
US-10-466-085A-16  
; Sequence 16, Application US/10466085A  
; Sequence 16, Application US/09932322

RESULT 17  
US-09-881-710-15  
; Sequence 15, Application US/09881710  
; Publication No. US20020086403A1  
; GENERAL INFORMATION:  
; APPLICANT: DESPRES, Philippe  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEUBEL, Vincent  
; APPLICANT: CATTEAU, Adeline  
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
; FILE REFERENCE: 200971050  
; CURRENT APPLICATION NUMBER: US/09/881,710  
; CURRENT FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: 60/212,129  
; PRIOR FILING DATE: 2000-06-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 15  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Dengue virus  
US-09-881-710-15

Query Match 30.3%; Score 30; DB 9; Length 20;  
Best Local Similarity 50.0%; Pred. No. 9.9e+02; Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGLWNNOQ 10  
Db 10 SSEGAWKHAQ 19

RESULT 18  
US-09-881-710-17  
; Sequence 17, Application US/09881710  
; Publication No. US20020086403A1  
; GENERAL INFORMATION:  
; APPLICANT: DESPRES, Philippe  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEUBEL, Vincent  
; APPLICANT: CATTEAU, Adeline

RESULT 19  
US-09-973-021-73  
Sequence 73, Application US/09973025  
Publication No. US20030182706A1  
GENERAL INFORMATION:  
APPLICANT: MARTEENS, GEERT  
BOSMAN, FONS  
DE MARTYNOFF, GUY  
BUYSE, MARIE ANGE  
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 110 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/973, 025  
FILING DATE: 10-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/612, 973  
FILING DATE: 11-Mar-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32, 205  
REFERENCE/DOCKET NUMBER: 1437-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-09-973-021-82  
Query Match  
Score 30; DB 9; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.9e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 6 WNNNQTOLFL 15  
Db 7 WGENDTDVFL 16  
RESULT 21  
US-09-839-303-73  
Sequence 73, Application US/05899303  
Publication No. US2003036110A1  
GENERAL INFORMATION:  
APPLICANT: MARTEENS, GEERT  
BOSMAN, FONS  
DE MARTYNOFF, GUY  
BUYSE, MARIE ANGE  
TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
FILE REFERENCE: 209671US0  
CURRENT APPLICATION NUMBER: US/09/881, 710  
CURRENT FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: 60/212, 129  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin version 3.1  
SEQ ID NO: 17  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Dengue virus  
US-09-881-710-17  
Query Match  
Score 30; DB 9; Length 20;  
Best Local Similarity 50.0%; Pred. No. 9.9e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 SSDGLWNNOQL 13  
Db 10 SSEGAWHQ 19  
RESULT 20  
US-09-973-025-82  
Sequence 82, Application US/09973025  
Publication No. US20020182706A1  
GENERAL INFORMATION:  
APPLICANT: MARTEENS, GEERT  
BOSMAN, FONS  
DE MARTYNOFF, GUY  
BUYSE, MARIE ANGE  
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 110 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/973, 025  
FILING DATE: 10-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/612, 973  
FILING DATE: 11-Mar-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32, 205  
REFERENCE/DOCKET NUMBER: 1437-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-09-973-025-82  
Query Match  
Score 30; DB 9; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.9e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 6 WNNNQTOLFL 15  
Db 7 WGENDTDVFL 16  
RESULT 21  
US-09-839-303-73  
Sequence 73, Application US/05899303  
Publication No. US2003036110A1  
GENERAL INFORMATION:  
APPLICANT: MARTEENS, GEERT  
BOSMAN, FONS  
DE MARTYNOFF, GUY  
BUYSE, MARIE ANGE  
TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
FILE REFERENCE: 209671US0  
CURRENT APPLICATION NUMBER: US/09/881, 710  
CURRENT FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: 60/212, 129  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin version 3.1  
SEQ ID NO: 17  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Dengue virus  
US-09-881-710-17  
Query Match  
Score 30; DB 9; Length 20;  
Best Local Similarity 38.5%; Pred. No. 9.9e+02;

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE  
 NUMBER OF SEQUENCES: 111  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHVE P.C.  
 STREET: 110 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/899, 303  
 FILING DATE: 06-JUL-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/612, 973  
 FILING DATE: 11-MAR-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BYRNE, THOMAS E.  
 REGISTRATION NUMBER: 32, 205  
 REFERENCE/DOCKET NUMBER: 1487-10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 816-4000  
 TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single

MOLECULE TOPLOGY: linear  
 MOLECULE TYPE: Peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
 ; US-09-899-303-73

Query Match 30.3%; Score 30; DB 10; Length 20;  
 Best Local Similarity 38.5%; Pred. No. 9.9e+02;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 SDGGLWNNTQQL 13  
 Db 7 NTNGQWHINSTAL 19

RESULT 22  
 US-09-899-303-82  
 Sequence 82, Application US/09899303  
 Publication No. US20010036110A1  
 GENERAL INFORMATION:  
 APPLICANT: MAERTENS, GEERT  
 BOSMAN, FONS  
 DE MARTYNOFF, GUY  
 BUYER, MARIE-ANGE  
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE  
 NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHVE P.C.  
 STREET: 110 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
 CURRENT FILING DATE: 2001-11-29  
 NUMBER OF SEQ ID NOS: 122  
 SOFTWARE: PatentIn 3.1  
 SEQ ID NO 73  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Hepatitis C virus  
 ; US-09-995-808-73

Query Match 30.3%; Score 30; DB 10; Length 20;  
 Best Local Similarity 38.5%; Pred. No. 9.9e+02;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 SDGGLWNNTQQL 13  
 Db 7 NTNGQWHINSTAL 19

RESULT 23  
 US-09-995-808-73  
 Sequence 73, Application US/09995808  
 Publication No. US20030095980A1  
 GENERAL INFORMATION:  
 APPLICANT: Imrogenetics N.V.  
 TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.  
 FILE REFERENCE: 2551-70  
 CURRENT FILING DATE: 2001-11-29  
 NUMBER OF SEQ ID NOS: 122  
 SOFTWARE: PatentIn 3.1  
 SEQ ID NO 73  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Hepatitis C virus  
 ; US-09-995-808-73

Query Match 30.3%; Score 30; DB 10; Length 20;  
 Best Local Similarity 38.5%; Pred. No. 9.9e+02;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 SDGGLWNNTQQL 13  
 Db 7 NTNGQWHINSTAL 19

RESULT 24  
 US-09-995-808-82  
 Sequence 82, Application US/09995808  
 Publication No. US20030095980A1  
 GENERAL INFORMATION:  
 APPLICANT: Imrogenetics N.V.  
 TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.  
 FILE REFERENCE: 2551-70  
 CURRENT FILING DATE: 2001-11-29  
 NUMBER OF SEQ ID NOS: 122  
 SOFTWARE: PatentIn 3.1

; SEQ ID NO: 82  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Hepatitis C virus  
; US-09-995-860-82

Query Match 30.3%; Score 30; DB 10; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.9e+02; Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNOTQFL 15  
Db 7 WGENDTDVFV 16

RESULT 25  
US-09-995-860-73  
; Sequence 73, Application US/09995860  
; Publication No. US20030118603A1  
; GENERAL INFORMATION:  
; APPLICANT: Imgenetics N.V.  
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and  
; TITLE OF INVENTION: therapeutic use.  
; FILE REFERENCE: 2551-69  
; CURRENT APPLICATION NUMBER: US/09/995, 860  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: Patentin 3.1

Query Match 30.3%; Score 30; DB 10; Length 20;  
Best Local Similarity 38.5%; Pred. No. 9.9e+02; Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SSDGLWNNOTQL 13  
Db 7 NTNGOWHINSTL 19

RESULT 26  
US-09-995-860-82  
; Sequence 82, Application US/09995860  
; Publication No. US20030118603A1  
; GENERAL INFORMATION:  
; APPLICANT: Imgenetics N.V.  
; TITLE OF INVENTION: purified hepatitis C virus envelope proteins for diagnostic and  
; TITLE OF INVENTION: therapeutic use.  
; FILE REFERENCE: 2551-68  
; CURRENT APPLICATION NUMBER: US/09/995, 791  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: Patentin 3.1

Query Match 30.3%; Score 30; DB 10; Length 20;  
Best Local Similarity 38.5%; Pred. No. 9.9e+02; Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SSDGLWNNOTQL 13  
Db 7 NTNGOWHINSTL 19

RESULT 27  
US-09-995-860-73  
; Sequence 73, Application US/09995791  
; Publication No. US20030147918A1  
; GENERAL INFORMATION:  
; APPLICANT: Imgenetics N.V.  
; TITLE OF INVENTION: purified hepatitis C virus envelope proteins for diagnostic and  
; TITLE OF INVENTION: therapeutic use.  
; FILE REFERENCE: 2551-68  
; CURRENT APPLICATION NUMBER: US/09/995, 791  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: Patentin 3.1

Query Match 30.3%; Score 30; DB 10; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.9e+02; Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNOTQFL 15  
Db 7 WGENDTDVFV 16

RESULT 28  
US-09-995-791-82  
; Sequence 82, Application US/09995791  
; Publication No. US20030147918A1  
; GENERAL INFORMATION:  
; APPLICANT: Imgenetics N.V.  
; TITLE OF INVENTION: purified hepatitis C virus envelope proteins for diagnostic and  
; TITLE OF INVENTION: therapeutic use.  
; FILE REFERENCE: 2551-68  
; CURRENT APPLICATION NUMBER: US/09/995, 791  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: Patentin 3.1

Query Match 30.3%; Score 30; DB 10; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.9e+02; Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNOTQFL 15  
Db 7 WGENDTDVFV 16

RESULT 29  
US-10-651-165-38  
; Sequence 38, Application US/10651165  
; Publication No. US2004004787A1  
; GENERAL INFORMATION:  
; APPLICANT: LEROUX-ROMIS, Geert  
; APPLICANT: DELEYS, Robert  
; APPLICANT: MAERTENS, Geert  
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C  
; TITLE OF INVENTION: VIRUS  
; FILE REFERENCE: 2551-94  
; CURRENT APPLICATION NUMBER: US/10/651, 65  
; CURRENT FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US/08/974, 690C  
; PRIOR FILING DATE: 1997-11-19  
; PRIOR APPLICATION NUMBER: PCT/EP94/03555  
; PRIOR FILING DATE: 1994-10-28  
; PRIOR APPLICATION NUMBER: EP 93402718.6  
; PRIOR FILING DATE: 1993-11-04

RESULT 27  
US-09-995-791-73

```

; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-38

Query Match          30.3%; Score 30; DB 15; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.9e+02; 4; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 4; SEQ ID NO: 15
Db      7 WGENUDTDVFV 16

RESULT 30
US-10-651-165-47
; Sequence 47, Application US/10651165
; Publication No. US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROBLS, Geert
; APPLICANT: DELBEY, Robert
; APPLICANT: MARTEENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELLS EPITOPE OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 47
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-47

Query Match          30.3%; Score 30; DB 15; Length 20;
Best Local Similarity 38.5%; Pred. No. 9.9e+02; 4; Mismatches 4; Indels 0; Gaps 0;
Matches 5; Conservative 4; Mismatches 4; SEQ ID NO: 13
Db      7 SSDGILWNNNQTL 19

RESULT 31
US-10-651-165-56
; Sequence 56, Application US/10651165
; Publication No. US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROBLS, Geert
; APPLICANT: DELBEY, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPE OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 19
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-56

Query Match          30.3%; Score 30; DB 15; Length 20;
Best Local Similarity 38.5%; Pred. No. 9.9e+02; 4; Mismatches 4; Indels 0; Gaps 0;
Matches 5; Conservative 3; Mismatches 5; SEQ ID NO: 13
Db      7 NXNGSSWHKNTAL 19

RESULT 32
US-10-634-895-15
; Sequence 15, Application US/10634895
; Publication No. US20040049016A1
; GENERAL INFORMATION:
; APPLICANT: DESPREZ, Philippe
; APPLICANT: COURAGGIER, Marie-Pierre
; APPLICANT: DEBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEINS
; FILE REFERENCE: 209671US0
; CURRENT APPLICATION NUMBER: US/10/634,895
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US/09/881,710
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 15
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dengue virus
US-10-634-895-15

Query Match          30.3%; Score 30; DB 15; Length 20;
Best Local Similarity 50.0%; Pred. No. 9.9e+02; 3; Mismatches 3; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 3; SEQ ID NO: 15
Db      7 NXNGSSWHKNTAL 19

```

Qy 1 SSDGJWNNNO 10  
Db 10 SSEGAWKHAQ 19

RESULT 33  
US-10-634-895-17  
; Sequence 17, Application US/10634895  
; Publication No. US20040049016A1  
; GENERAL INFORMATION:  
; APPLICANT: DESPRES, Philippe  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEUBEL, Vincent  
; APPLICANT: CATTEAU, Adeline  
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
; FILE REFERENCE: 209671US0  
; CURRENT APPLICATION NUMBER: US/10/634,895  
; CURRENT FILING DATE: 2003-08-06  
; PRIOR APPLICATION NUMBER: US/09/881,710  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/212,129  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 17  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Dengue virus  
; US-10-634-895-17

Query Match 30.3%; Score 30; DB 15; Length 20;  
Best Local Similarity 50.0%; Pred. No. 9.9e+02; Mismatches 5; Conservative 5; Indels 0; Gaps 0;  
Matches 5; Conservatve 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGJWNNNO 10  
Db 10 SSEGAWKHAQ 19

RESULT 34  
US-10-311-213-22  
; Sequence 22, Application US/10311213  
; Publication No. US20040101862A1  
; GENERAL INFORMATION:  
; APPLICANT: DESPRES, Philippe  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEUBEL, Vincent  
; APPLICANT: CATTEAU, Adeline  
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
; FILE REFERENCE: 231164US0CT  
; CURRENT APPLICATION NUMBER: US/10/311,213  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: PCT/IB01/01570  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn 3.1  
; SEQ ID NO: 82  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Hepatitis C virus  
; US-10-311-213-22

Query Match 30.3%; Score 30; DB 16; Length 20;  
Best Local Similarity 50.0%; Pred. No. 9.9e+02; Mismatches 5; Conservative 5; Indels 0; Gaps 0;  
Matches 5; Conservatve 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGJWNNNO 10  
Db 10 SSEGAWKHAQ 19

RESULT 35  
US-10-321-798-73  
; Sequence 73, Application US/10321798  
; Publication No. US20040126395A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.  
; FILE REFERENCE: 2551-93  
; CURRENT APPLICATION NUMBER: US/10/321,798  
; CURRENT FILING DATE: 2003-12-18  
; PRIOR APPLICATION NUMBER: 60/418,358  
; PRIOR FILING DATE: 2002-10-16  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn 3.1  
; SEQ ID NO: 73  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Hepatitis C virus  
; US-10-321-798-73

Query Match 30.3%; Score 30; DB 16; Length 20;  
Best Local Similarity 38.5%; Pred. No. 9.9e+02; Mismatches 5; Conservative 4; Indels 0; Gaps 0;  
Matches 5; Conservatve 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SSDGJWNNNQTL 13  
Db 7 NTNGGWHINSTAL 19

RESULT 36  
US-10-321-798-82  
; Sequence 82, Application US/10321798  
; Publication No. US20040126395A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.  
; FILE REFERENCE: 2551-93  
; CURRENT APPLICATION NUMBER: US/10/321,798  
; PRIOR APPLICATION NUMBER: 60/418,358  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 10/020,510  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn 3.1  
; SEQ ID NO: 82  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Hepatitis C virus  
; US-10-321-798-82

Query Match 30.3%; Score 30; DB 16; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.9e+02; Mismatches 4; Conservative 4; Indels 0; Gaps 0;  
Matches 4; Conservatve 4; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNNQTLFL 15  
Db 7 WGENDTDVVF 16

RESULT 37  
US-09-563-222-53  
; Sequence 53, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS

; FILE REFERENCE: 310098\_406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-563-222-53

Query Match 29.3%; Score 29; DB 10; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.5e+06; Matches 4; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 DLGMNNN 9  
Db 2 GYWNNS 7

; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: AU PR 2919  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 678  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 557  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Bacillus halodurans  
; US-10-416-249-557

Query Match 29.3%; Score 29; DB 16; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03; Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 DGLMNNNQQLF 14  
Db 4 EGLDEBNQSLF 15

RESULT 38  
US-10-783-950-53  
; Sequence 53; Application US/10783950  
; Publication No. US20040199945A1  
; GENERAL INFORMATION:  
; APPLICANT: EPICTIVE PHARMACEUTICALS, INC.  
; APPLICANT: HIAINT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/10/783, 950  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US/09/563, 222  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/563, 222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-10-783-950-53

RESULT 40  
US-10-416-249-563  
; Sequence 53; Application US/10416249  
; Publication No. US20040132121A1  
; GENERAL INFORMATION:  
; APPLICANT: DALTRYMPLE, Brian P.  
; APPLICANT: Kongswan, Kritaya  
; APPLICANT: Wijffels, Gene L.  
; APPLICANT: Jennings, Philip A.  
; APPLICANT: Kemp, Gregory W.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING ANTIBACTERIAL  
; FILE REFERENCE: CULM42\_001APC  
; CURRENT APPLICATION NUMBER: US/10/416, 249  
; CURRENT FILING DATE: 2003-11-10  
; PRIOR APPLICATION NUMBER: PCT/AU01/01436  
; PRIOR FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: AU PR 1320  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: AU PR 2919  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 678  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 563  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Listeria innocua  
; US-10-416-249-563

Query Match 29.3%; Score 29; DB 16; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03; Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 DGLMNNNQQLF 14  
Db 4 EGLDEBNQSLF 15

Query Match 29.3%; Score 29; DB 17; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.5e+06; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 DLGMNNN 9  
Db 2 GYWNNS 7

Query Match 29.3%; Score 29; DB 16; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03; Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 DGLMNNNQQLF 14  
Db 4 EGLDEBNQSLF 15

Search completed: December 30, 2004, 16:43:26  
Job time : 144 secs

Copyright (c) 1993 - 2004 Compugen Ltd.  
 OM protein - protein search, using sw model  
 Run on: December 30, 2004, 16:22:44 ; Search time 38 Seconds  
 (without alignments)  
 45.576 Million cell updates/sec

103 18 18.2 9 2 D28854 fibrinopeptide B -  
104 18 18.2 9 2 PT0238 Ig heavy chain CRD  
105 18 18.2 9 2 PT0272 Ig heavy chain CRD  
106 18 18.2 10 2 PQ0753 beti-fructofuranos  
107 18 18.2 11 2 PH0914 T-cell receptor be  
108 18 18.2 11 2 S04875 nifs protein - Bra  
109 18 18.2 12 2 A29169 phospholipase A2 -  
110 18 18.2 12 2 S68271 major urinary prot  
111 18 18.2 12 2 PT0216 T-cell receptor be  
112 18 18.2 12 2 S28215 glucose endo-1,3-be  
113 18 18.2 12 2 A49637 MHC class II histo  
114 18 18.2 13 2 S47358 T-cell antigen rec  
115 18 18.2 14 2 PT0077 proteochondroitin c  
116 18 18.2 14 2 S1766 beta-glucosidase (lectin Bl - Pboho  
117 18 18.2 14 2 PR0007 scotrophobin - rat  
118 18 18.2 15 1 SFR7 troponin - rabbit  
119 18 18.2 15 2 I46512 Ig heavy chain DJ  
120 18 18.2 15 2 PH1366 T-cell receptor al  
121 18 18.2 15 2 PH0782 transfroming prote  
122 18 18.2 16 2 A46236 tropom - rabbit  
123 18 18.2 17 2 I46511 gindipain. 44K - P  
124 18 18.2 17 2 E53113 seed protein ws-2  
125 18 18.2 17 2 B61491 adherence lectin 1  
126 18 18.2 17 2 B31435 hypothetical prote  
127 18 18.2 17 2 C84063 hypothetical CORI/  
128 18 18.2 17 2 I76573 T-cell receptor be  
129 18 18.2 18 2 B48839 hypothetical prote  
130 18 18.2 18 2 H64711 myosin heavy chain  
131 18 18.2 18 2 I50389 hypothetical PML/R  
132 18 18.2 18 2 I54078 caprid protein VP2  
133 18 18.2 19 2 P00548 anti-bacterial prot  
134 18 18.2 19 2 S74087 pre-T/NK cell-assb  
135 18 18.2 19 2 I39327 insulin-like growt  
136 18 18.2 20 2 PN0115 calpain (EC 3.4.22  
137 18 18.2 20 2 S32502 Ig heavy chain DJ  
138 18 18.2 20 2 PH1326 defensin AMP2 - Da  
139 18 18.2 20 2 S66222 periplasmic flagel  
140 18 18.2 20 2 B44913 major outer membran  
141 18 18.2 20 2 S28435 agglutinin beta-2  
142 18 18.2 20 2 S03987 seed protein ws-20  
143 18 18.2 20 2 E61497 T-cell receptor be  
144 17 17.2 6 2 PT0519 T-cell receptor be  
145 17 17.2 7 2 PT0688 T-cell receptor be  
146 17 17.2 8 2 PT0724 urine glycopeptide  
147 17 17.2 8 2 XGHUEU fibrinogen beta ch  
148 17 17.2 9 2 C24180 L-hybosorin - ja  
149 17 17.2 9 2 A45199 glutathione transf  
150 17 17.2 10 2 S71868

## ALIGNMENTS

**RESULT 1**

F49039 T-cell receptor beta chain V-D-J-C region (V beta 2, J beta 1.5) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997

C;Accession: F49039

R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.

Bur. J. Immunol. 22, 541-549, 1992 Variation in human T cell receptor V beta and J beta repertoire: analysis using T-cell receptor beta chain (V beta 2, J beta 1.5) - human (fragment)

A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using T-cell receptor beta chain (V beta 2, J beta 1.5) - human (fragment)

A;Reference: Variance number: A49039; MUID:92164737; PMID:1311263

A;Accession: F49039

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-16 <ROS>

A;Note: sequence extracted from NCBI backbone (NCBIP:90718)

C;Keywords: T-cell receptor

Query Match 31.3%; Score 31; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 86; Indels 7; Gaps 0;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQTLF 14  
|:||:||:||:  
DB 2 SASGTDNSNQPQHF 15

RESULT 2

I49422 L-lactate dehydrogenase (EC 1.1.1.27) chain X - western wild mouse (fragment)

N;Alternate names: lactate dehydrogenase C

C;Species: Mus spretus (western wild mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I49422

R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H. Mamm. Genome 5, 349-355, 1994

A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A;Reference number: I48934; MUID:94319082; PMID:8043949

A;Accession: I49422

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-19 <RES>

A;Cross-references: UNIPROT:Q62545; EMBL:U05739; NID:9497076; PIDN:AAB60478.1; PID:94970

C;Superfamily: L-lactate dehydrogenase

C;Keywords: oxidoreductase

QY 1 SSDGIVNN 7  
|:||:||:  
Db 6 SADTILW 12

Query Match 30.3%; Score 30; DB 2; Length 19;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 1; Gaps 0;

QY 1 SSDGIVNN 7  
|:||:||:  
Db 6 SADTILW 12

RESULT 3

PQ0300 large protein - bovine respiratory syncytial virus (strain A51908) (fragment)

C;Species: bovine respiratory syncytial virus

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004

C;Accession: PQ0300

R;Zamora, M.; Samal, S.K. J. Gen. Virol. 73, 737-741, 1992

A;Title: Sequence analysis of B2 mRNA of bovine respiratory syncytial virus obtained from A;Reference number: JQ1481; MUID:92185490; PMID:1312130

A;Accession: PQ0300

A;Molecule type: mRNA

A;Residues: 1-20 <ZAM>

A;Cross-references: UNIPROT:Q65705; UNIPROT:Q8V686; GB:MB2816; NID:9210823; PIDN:AAA4280

C;Genetics: L

Query Match 27.3%; Score 27; DB 2; Length 20;  
Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 3; Mismatches 7; Gaps 0;

QY 3 DGLWMNNNTQTLFLEHS 18  
|:||:||:||:||:  
Db 2 DTLHENSTNVILIDS 17

RESULT 4

PT049 T-cell receptor beta chain (B83) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C;Accession: PH0749

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.J. J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>  
A;Cross-references: EMBL:X60840; NID:950116; PIDN:CAA43233.1; PID:950117  
A;Experimental source: T lymphocyte  
C;Keywords: T-cell receptor

Query Match 25.3%; Score 26; DB 2; Length 16;  
Best Local Similarity 71.4%; Pred. No. 5.4e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 NNGTQOLF 14  
Db 9 NNGTQOLF 15

RESULT 5

I46654 T-cell receptor delta-chain J-delta-3 - pig (fragment)  
C;Species: Sus scrofa domesticus (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 05-Nov-1999  
C;Accession: I46654  
R;Yan, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.  
J. Immunol. 155, 1981-1993, 1995  
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old  
A;Reference number: I46623; MUID:9536165; PMID:7636249  
A;Accession: I46654  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-19 <IAN>  
A;Cross-references: GB:D49562; NID:91041176; PIDN:BA08506.1; PID:91041177  
C;Keywords: T-cell receptor

Query Match 26.3%; Score 26; DB 2; Length 19;  
Best Local Similarity 35.3%; Pred. No. 6.5e+02; Mismatches 2; Indels 6; Gaps 1;  
Matches 6; Conservative 3; Mismatches 2; Indels 6; Gaps 1;

QY 6 WNNNQ-----TQTLIE 16  
Db 2 WDTRQMYFGAGTKLVE 18

RESULT 6

PH0138 T-cell receptor beta chain V-D-J region C8 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 30-May-1997  
C;Accession: PH0138  
R;Martin, R.; Howell, M.D.; Jaraguemada, D.; Flerlage, M.; Richert, J.; Brostoff, S.; Ig J. Exp. Med. 173, 19-24, 1991  
A;Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context of a major histocompatibility complex class II molecule  
A;Reference number: PH0135; MUID:91086843; PMID:1702137  
A;Accession: PH0138  
A;Molecule type: mRNA  
A;Residues: 1-13 <MAR>  
C;Keywords: T-cell receptor

Query Match 26.3%; Score 25; DB 2; Length 13;  
Best Local Similarity 60.0%; Pred. No. 6.2e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNNNQ 10  
Db 7 WTNNB 11

RESULT 7

PT0589 T-cell receptor beta chain V-D-J region (141-1A) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C;Accession: PT0589  
C;Accession: PT0589  
C;Accession: PT0589  
R;Reehey, A.J.; Pichler, J.; Loh, H.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire.  
A;Reference number: PH0746; MUID:92078846; PMID:1836010  
A;Accession: PH0756  
A;Molecule type: mRNA  
A;Residue: 1-13 <CAS>  
A;Cross-references: EMBL:X60850; NID:951482; PIDN:CAA43241.1; PID:951483  
A;Experimental source: T lymphocyte  
C;Keywords: T-cell receptor

Query Match 24.2%; Score 24; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 8.9e+02; Mismatches 3; Indels 4; Gaps 1;  
Matches 7; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

QY 1 SSDGLWNNTQOLF 14  
Db 3 SGDGLWNNTQOLF 12

RESULT 10

PC1299 Subtilisin (EC 3.4.21.62) GX - Bacillus sp. (strain 6644) (Fragment)

A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0589  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <PFB>  
A;Experimental source: day 19 fetal thymus, strain BALB/C  
A;Keywords: T-cell receptor

Query Match 24.2%; Score 24; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSDGL 5  
Db 2 SSDGL 6

RESULT 8

S23370 T-cell receptor alpha chain J region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C;Accession: S23370  
C;Plausible: S23370  
R;Pluschke, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman Bur. J. Immunol. 21, 2749-2754, 1991  
A;Title: Biased T cell receptor, V(alpha) region repertoire in the synovial fluid of rheumatoid arthritis  
A;Reference number: S23364; MUID:92037820; PMID:1657615  
A;Accession: S23370  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residue: 1-10 <PLU>  
A;Cross-references: EMBL:X58165  
C;Keywords: T-cell receptor

Query Match 24.2%; Score 24; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 6.7e+02; Mismatches 0; Indels 0; Gaps 0;

QY 6 WNNN 9  
Db 3 WDNN 6

C;Species: *Bacillus* sp.  
C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: P01299  
C;Species: *Anguilla japonica* (Japanese eel)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C;Accession: JH0253  
R;Durham, D.R.  
Bloch. Biophys. Res. Commun. 194, 1365-1370, 1993  
A;Reference number: P01299; MUID:93356814; PMID:8352796  
A;Molecule type: protein  
A;Residues: 1-16 <DPS>  
A;Cross-references: UNIPROT:Q9R557  
C;Keywords: hydrolase; serine protease

Query Match 24.2%; Score 24; DB 2; Length 16;  
Best local Similarity 42.9%; Pred. No. 1.1e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 WNNNOTQ 12  
Db 5 WGDNRVQ 11

RESULT 11

S27351  
lysophospholipase - human  
C;Species: *Homo sapiens* (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S27351  
R;Garrett, D.; Holtzberg, F.; Steiner, M.R.; Egan, R.W.; Clark, M.A.

Bloch, J. 288, 831-837, 1992  
A;Title: Butyric acid-induced differentiation of HL-60 cells increases the expression of

A;Reference number: S27350; MUID:93111958; PMID:1471998  
A;Accession: S27351

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <GAK>  
A;Cross-references: UNIPROT:P56643

Query Match 24.2%; Score 24; DB 2; Length 20;  
Best local Similarity 35.7%; Pred. No. 1.4e+03;  
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SSDGLWNNGTQOLF 14  
Db 2 ASISLYNSNTSYF 15

RESULT 12

S30763  
S-adenosyl-L-methionine decarboxylase alpha chain - *Acanthamoeba castellani*  
C;Species: *Acanthamoeba castellani*

C;Date: 08-Jun-1994 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C;Accession: S30763  
R;Hogg, E.R.; Byers, T.J.

Bloch, J. 295, 203-209, 1993  
A;Title: S-Adenosyl-L-methionine decarboxylase of *Acanthamoeba castellani* (Neff): purif

A;Reference number: S30763; MUID:94029912; PMID:8216217  
A;Accession: S30763

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <RG>  
A;Cross-references: UNIPROT:P34039

Query Match 23.7%; Score 23.5; DB 2; Length 20;  
Best local Similarity 43.8%; Pred. No. 1.7e+03;  
Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SSDGLWNNGTQOLF 16  
Db 2 SSMEVWN---TKLILK 14

JH0253

gut pentapeptide - Japanese eel  
C;Species: *Anguilla japonica* (Japanese eel)

C;Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 09-Jul-2004

C;Accession: A41117  
R;Durham, D.R.; Weise, C.; Raba, R.; Havikaar, A.; Huchó, F.

R;Kreienkamp, H.J.; Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from *Torpedo* ar

A;Reference number: A41117; MUID:91296772; PMID:2068091  
A;Accession: A41117  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <RKE>  
A;Cross-references: UNIPROT:Q7LZ22  
C;Keywords: carboxylic ester hydrolase

Query Match 23.2%; Score 23; DB 2; Length 8;  
Best local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LWNNN 9

RESULT 13

Db : |||  
4 MWNPN 8

RESULT 16  
 Ig heavy chain DJ region (clone C100-91A) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 10-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PH1344  
 C;Molecule type: DNA  
 A;Residues: 1-10 <WAS>  
 C;Keywords: heterotetramer; immunoglobulin  
 Query Match 23.2%; Score 23; DB 2; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 9.6e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SGDWN 6  
 Db 2 SDGDN 6

RESULT 17  
 proboscipedia - fruit fly (*Drosophila pseudoobscura*) (fragment)  
 C;Species: *Drosophila pseudoobscura*  
 C;Accession: A44874  
 C;Date: 31-May-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 R;Randazzo, F.M.; Cribs, D.L.; Kaufman, T.C.  
 Development 113, 257-271, 1991  
 A;Title: Rescue and regulation of *proboscipedia*: a homeotic gene of the Antennapedia Complex  
 A;Reference number: A44874; MUID:92111389; PMID:1684932  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Accession: A44874  
 A;Note: sequence extracted from NCBR backbone (NCBIN:77929, NCBIB:77931)  
 C;Genetic ID: FlyBase:Dpse/pb  
 A;Cross-references: Flybase:FBgn00212734  
 C;Superfamily: unassigned homeobox proteins; homeobox homology  
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 23.2%; Score 23; DB 2; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 WNNN 9  
 Db 5 WGNN 8

RESULT 18  
 C56211  
 progesterone receptor-related protein p23 - rabbit (fragment)  
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)  
 C;Accession: C56211  
 C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 20-Jun-2000  
 R;Johnson, J.L.; Beato, T.G.; Krco, C.J.; Toft, D.O.  
 Mol. Cell. Biol. 14, 1956-1963, 1994  
 A;Title: Characterization of a novel 23-kilodalton protein of inactive progesterone receptor  
 A;Reference number: A56211; MUID:94158868; PMID:8114727  
 A;Accession: C56211  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-18 <OH>  
 C;Superfamily: steroid hormone receptor  
 C;Keywords: steroid hormone receptor

Query Match 23.2%; Score 23; DB 2; Length 18;  
 Best Local Similarity 27.3%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNQTQFLF 16  
 Db 8 WYDRDYVFF 18

RESULT 19  
 A61211  
 anantin - *Streptomyces coeruleescens*  
 C;Species: *Streptomyces coeruleescens*  
 C;Date: 03-May-1994 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
 C;Accession: A61211  
 C;Accession: A61211  
 R;Wiers, D.F.; Lahm, H.W.; Maenneberg, M.; Labhardt, A.M.  
 J. Antibiot. 44, 172-180, 1991  
 A;Title: Anantin -- a peptide antagonist of the atrial natriuretic factor (ANF). II. Determination of the structure  
 A;Reference number: A61211; MUID:91185186; PMID:1826288  
 A;Accession: A61211  
 A;Molecule type: protein  
 A;Residues: 1-17 <WYS>  
 A;Cross-references: UNIPROT:Q7M0J9  
 A;Note: the isopeptide linked residue 8 is shown as Asn rather than Asp  
 P;1-8/Cross-link: isopeptide amino end (Gly-Asn) #status experimental

Query Match 23.2%; Score 23; DB 2; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 WNNN 9  
 Db 5 WGNN 8

RESULT 20  
 C56211  
 progesterone receptor-related protein p23 - rabbit (fragment)  
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)  
 C;Accession: C56211  
 C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 20-Jun-2000  
 R;Johnson, J.L.; Beato, T.G.; Krco, C.J.; Toft, D.O.  
 Mol. Cell. Biol. 14, 1956-1963, 1994  
 A;Title: Characterization of a novel 23-kilodalton protein of inactive progesterone receptor  
 A;Reference number: A56211; MUID:94158868; PMID:8114727  
 A;Accession: C56211  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-18 <OH>  
 C;Superfamily: steroid hormone receptor  
 C;Keywords: steroid hormone receptor

Query Match 23.2%; Score 23; DB 2; Length 18;  
 Best Local Similarity 27.3%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNQTQFLF 16  
 Db 8 WYDRDYVFF 18

RESULT 21  
 A44854  
 L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.-) - *Acinetobacter calcoaceticus* (fragment)  
 N;Alternate names: DABA decarboxylase  
 C;Species: *Acinetobacter calcoaceticus*  
 C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C;Accession: A44854; A1817  
 R;Yamamoto, S.; Iizuka, Y.; Tougou, K.; Shinoda, S.  
 J. Gen. Microbiol. 138, 1461-1465, 1992  
 A;Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from *A.*

A;Reference number: A44854; MUID:92381494; PMID:1512577

A;Accession: A44854

A;Molecule type: protein

A;Residues: 1-19 <YAM>

A;Cross-references: UNIPROT:Q9R519

A;Experimental source: ATCC 23055

A;Note: sequence extracted from NCBI backbone (NCBIP:112331)

C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 23.2%; Score 23; DB 2; Length 19;

Best Local Similarity 42.9%; Pred. No. 2e+03;

Mismatches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 11 LWNDAES 17

RESULT 22

S16202 5 LWNMQQT 11

pyrrole-5-carboxylate reductase - soybean chloroplast

C;Species: chloroplast Glycine max (soybean)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997

C;Accession: S16202

R;Chilson, O. P.; Kelly-Chilson, A.E.; Siegel, N.R.

Arch. Biochem. Biophys. 288, 350-357, 1991

A;Title: Pyrrole-5-carboxylate reductase in soybean nodules: isolation/partial primary

A;Reference number: S16202; MUID:91378472; PMID:1898034

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-20 <ARC>

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 23.2%; Score 23; DB 2; Length 20;

Best Local Similarity 30.0%; Pred. No. 2.1e+03;

Mismatches 4; Conservative 3; Indels 0; Gaps 0;

Db 7 AEGQWRRDDVT 16

RESULT 23

S55756 link protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Mar-1999

C;Accession: S55756

R;Rhodes, C.; Yamada, Y.

Nucleic Acids Res. 23, 2305-2313, 1995

A;Title: Characterization of a glucocorticoid responsive element and identification of a

A;Reference number: S55756; MUID:95334387; PMID:7610060

A;Accession: S55756

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-20 <RHO>

A;Cross-references: EMBL:X55057

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1991

Query Match 23.2%; Score 23; DB 2; Length 20;

Best Local Similarity 60.0%; Pred. No. 2.1e+03;

Mismatches 3; Conservative 1; Indels 0; Gaps 0;

Db 6 WNNNQ 10

16 WNSGQ 20

RESULT 25

PH1471 6 WNNNQ 10

T-cell receptor beta chain (clone A24/PEP4) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 15-Mar-2004

C;Accession: PH1471

R;Casanova, J.L.; Martinon, P.; Gournier, H.; Barra, C.; Pannatier, C.; Regnault, A.; Koenig, J.

J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatibility antigens

A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1471

A;Molecule type: mRNA

A;Residues: 1-14 <CAS>

A;Experimental source: cytolytic T-lymphocyte

C;Keywords: receptor; T-cell

Query Match 22.2%; Score 22; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 2e+03;

Mismatches 4; Conservative 1; Indels 0; Gaps 0;

Db 7 NNNCOPLF 14

6 DNQDITQYE 13

RESULT 26

G49655

T-cell-receptor beta chain variable region (clone 1) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997

C;Accession: G49655; RA9555; A46655

R;Grom, A.A.; Thompson, S.D.; Luyrink, L.; Passo, M.; Choi, E.; Glass, D.N.

Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993

A;Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juvenile

A;Reference number: A49655; MUID:94068553; PMID:8248215

A;Accession: G49655

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-15 <GR1>

A;Experimental source: hip joint, synovial tissues

A;Note: this was designated clone 1

A;Cross-references: F49655

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-15 <GR2>

A;Experimental source: hip joint, synovial tissues

A;Note: sequence extracted from NCBI backbone (NCBIP:140451)

A;Accession: A49655

A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-15 <GRO>  
A;Experimental source: knee joint, synovial fluid lymphocytes  
A;Note: this was designated clone SF-1  
A;Reference: sequence extracted from NCBI backbone (NCBIP:140445)  
C;Keywords: T-cell receptor

Query Match 22.2%; Score 22; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03; Mismatches 5; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 5;

QY 1 SSDGLWNNNQ 10  
Db 5 SPDAGWTDQ 14

RESULT 27

B45474 thrombospondin 2 - bovine (fragment)  
NI:Alternate names: corticotropin-induced secreted protein (CISP); thrombospondin homolog  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: B45474  
R;Pellerin, S.; Lafeuillade, B.; Scherrer, N.; Gagnon, J.; Shi, D.L.; Chambaz, E.M.; Feil, J. Biol. Chem. 268, 4301-4310, 1993  
A;Title: Corticotropin-induced secreted protein, an ACTH-induced protein secreted by adr  
A;Reference number: A45474; MUID:93179438; PMID:8382699  
A;Accession: B45474  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <PEL>  
A;Cross-references: UNIPROT:09TS97  
A;Experimental source: adrenocortical cells  
A;Note: sequence extracted from NCBI backbone (NCBIP:125842)

Query Match 22.2%; Score 22; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.2e+03; Mismatches 1; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 NNGTQ 12  
Db 2 NNGAQ 6

RESULT 28

S57519 T cell receptor beta chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 10-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
C;Accession: S57519  
R;Burrows, S.R.; Siline, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaez, V.P.  
Submitted to the EMBL Data Library, June 1995  
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified by reference number: S57519  
A;Accession: S57519  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Cross-references: EMBL:Z49930; NID:9887494; PIDN:CAA90176.1; PID:9887495  
C;Keywords: T-cell receptor

Query Match 22.2%; Score 22; DB 2; Length 17;  
Best Local Similarity 42.9%; Pred. No. 2.5e+03; Mismatches 6; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SSDGLWNNNQQLF 14  
Db 3 SSQGLISISSVQYF 16

RESULT 29

S57556 Query Match 22.2%; Score 22; DB 2; Length 19;

Best Local Similarity 41.7%; Pred. No. 2.8e+03; Mismatches 5; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches+03; Indels 0; Gaps 0;

Qy 1 SSDGLWNNTQ 12  
Db 8 SLDVENNEWWRK 19

RESULT 32

I40063 shikimate 5-dehydrogenase (EC 1.1.1.25) - *Buchnera aphidicola* (fragment)

C;Species: *Buchnera aphidicola*  
C;Accession: I40063  
A;Title: Characterization of a putative 23S rRNA operon of *Buchnera aphidicola* (endosymbiont)  
A;Reference number: I40061; MUID:9521214; PMID:535281  
A;Accession: I40063  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-19 <RES>  
A;Cross-references: UNIPROT:Q44609; EMBL:U10497; NID:9854713; PIDN:AAA79126.1; PID:9854713  
C;Genetics:  
A;Gene: aroE  
C;Keywords: oxidoreductase

Query Match 22.2%; Score 22; DB 2; Length 19;  
Best Local Similarity 75.0%; Pred. No. 2.8e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LWNN 8  
Db 4 LWND 7

RESULT 33

H22565 R-phycocerythrin gamma-C chain - red alga (*Gastroclonium coulteri*) (fragment)

C;Species: *Gastroclonium coulteri*  
C;Accession: H22565  
A;Title: Characterization of the bilin attachment sites in R-phycocerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Molecule type: protein  
R;Klotz, A.V.; Glaser, A.N.  
J. Biol. Chem., 260, 485-4863, 1985  
A;Residues: 1-20 <KLO>  
A;Cross-references: UNIPROT:07M270  
C;Superfamily: Aglaothamnion neglectum R-phycocerythrin gamma chain 33

Query Match 22.2%; Score 22; DB 2; Length 20;  
Best Local Similarity 37.5%; Pred. No. 3e+03; Mismatches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 7 MNMQOLP 14  
Db 8 HHEETQIF 15

RESULT 34

A39308 glycine reductase (EC 1.4.99.-) sulfhydryl protein C, alpha chain - *Clostridium sticklandii*

C;Species: *Clostridium sticklandii*  
C;Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 09-Jul-2004  
C;Accession: A39308  
R;Stadtman, T.C.; Davis, J.N.  
J. Biol. Chem., 266, 22147-22153, 1991  
A;Title: Glycine reductase protein C. Properties and characterization of its role in the  
A;Reference number: A39308; MUID:92042141; PMID:1939235  
A;Accession: A39308  
A;Status: preliminary

Query Match 21.2%; Score 21; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.5e+03; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GLWN 7  
Db 5 LWN 7

RESULT 35

PT0562 T-cell receptor beta chain V-D-J region (I126-IAK) - mouse (fragment)

C;Species: *Mus musculus* (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0562  
R;Feeney, A.J.  
J. Exp. Med., 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-9 <FFEE>  
A;Experimental source: day 18 fetal thymus, strain BALB/C  
C;Keywords: T-cell receptor

Query Match 21.2%; Score 21; DB 2; Length 9;  
Best Local Similarity 65.7%; Pred. No. 2.8e+05; Mismatches 2; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSDGLW 6  
Db 2 SSDDNW 7

RESULT 36

PH1308 Ig heavy chain DJ region (clone C731-94) - human (fragment)

C;Species: *Homo sapiens* (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: PH1308  
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med., 176, 157-1581, 1992  
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphocytes  
A;Reference number: PH1302; MUID:93094761; PMID:1460419  
A;Accession: PH1308  
A;Molecule type: DNA  
A;Residues: 1-12 <WAS>  
A;Keywords: heterotetramer; immunoglobulin

Query Match 21.2%; Score 21; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 2.5e+03; Mismatches 1; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLWN 7  
Db 5 GWN 11

RESULT 37

S57572 T cell receptor V-J junctional alpha chain region - human (fragment)

C;Species: *Homo sapiens* (man)  
C;Date: 19-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
C;Accession: S57572  
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaez, V.P.

submitted to the EMBL Data Library. June 1995  
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified to

A;Reference number: S57494

A;Accession: 557572

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-14 <BUR>

A;Cross-references: EMBL:249957; NID:9887478; PID:CAA90228.1; PID:9887479

C;Keywords: T-cell receptor

Query Match 21.2%; Score 21; DB 2; Length 14;

Best Local Similarity 33.3%; Pred. No. 2.9e+03; Mismatches 4;

Matches 3; Conservative 2; Mismatches 4;

Qy 6 WNNNQQLF 14

Db 5 WSGNTPLVF 13

RESULT 38

PH194 Ig H chain V-D-J region (wild-type clone 149) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Accession: PH194 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 3179, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1594

A;Molecule type: DNA

A;Residues: 1-14 <URV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 21.2%; Score 21; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.9e+03; Mismatches 0;

Matches 3; Conservative 0; Mismatches 0;

Qy 4 GLW 6

Db 11 GLW 13

RESULT 39

A59046 alpha-conotoxin MII - cone shell (Conus magus)

C;Species: Conus magus (magus cone)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: A59046

R;Cartier, G.B.; Yoshikami, D.; Gray, W.R.; Ito, S.; Olivera, B.M.; McIntosh, J.M.

J. Biol. Chem. 271, 752-758, 1996

A;Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine receptor

A;Reference number: A59046; MUID:96205934; PMID:8631783

A;Accession: A59046

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <CAR>

A;Cross-references: UNIPROT:P56636

C;Superfamily: alpha-conotoxin

C;Keywords: Acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot

F;1-16/Product: alpha-conotoxin MII #status experimental <MAT>

F;1-8,3-16/Disulfide bond: #status experimental

F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 21.2%; Score 21; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.4e+03; Mismatches 4;

Matches 4; Conservative 0; Mismatches 0;

Qy 15 LEHS 18

Db 10 LEHS 13

RESULT 40

S28213 Glutathione transferase (EC 2.5.1.18) - European toad (fragments)

C;Species: Bufo bufo (European toad)

C;Accession: S28213 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999

R;Aceto, A.; Dragani, B.; Buccarelli, T.; Sacchetta, P.; Martini, F.; Angelucci, S.; Am

Biochem. J. 289, 417-422, 1993

A;Title: Purification and characterization of the major glutathione transferase from adu

A;Reference number: S28213; MUID:93143709; PMID:8424786

A;Molecule type: protein

A;Residues: 1-16 <KEB>

A;Experimental source: liver

C;Keywords: transferase

Query Match 21.2%; Score 21; DB 2; Length 16;

Best Local Similarity 45.5%; Pred. No. 3.4e+03; Mismatches 5;

Matches 5; Conservative 1; Mismatches 3;

Indels 2; Gaps 1;

Qy 6 WNNNQQLF 16

Db 4 WDNEAN-PLE 12

Search completed: December 30, 2004, 16:32:07

Job time : 40 secs

*This Page Blank (uspto)*

Copyright (c) 1993 - 2004 CompuGen Ltd.

GenCore version 5.1.6

OM protein - protein search, using bw model

Run on: December 30, 2004, 16:14:44 ; Search time 188 Seconds  
(without alignments)  
55.089 Million cell updates/sec

Title:	US-10-718-321-1			
Perfect score:	99			
Sequence:	1 SSDGLWNNTQLFLEHS 18			
Scoring table:	BLOSUM62			
	Gapp 10.0 , Gapext 0.5			
Searched:	1825181 seqs, 575374646 residues			
Total number of hits satisfying chosen parameters:	14317			
Minimum DB seq length:	0			
Maximum DB seq length:	20			
Post-processing:	Minimum Match 0%			
	Maximum Match 100%			
Database :	UniProt 02:*			
	1: uniprot_sprot:*			
	2: uniprot_trembl:*			
<b>SUMMARIES</b>				
Result No.	Score	Query Length	DB ID	Description
1	30	30.3	19 2	Q62545 mus spretus
2	27	27.3	20 2	Q65705 bovine resp
3	27	27.3	20 2	Q8v686 bovine resp
4	26	26.3	17 2	Q78378 human immun
5	26	26.3	19 2	Q9ETX8 helicobacte
6	26	26.3	20 2	Q6SY55 drosophila
7	26	26.3	20 2	AAR84726 drosophil
8	25	25.3	10 2	Q9TR47 bos taurus
9	25	25.3	19 2	Q15610 homo sapien
10	25	25.3	19 2	Q9ETX7 helicobacte
11	25	25.3	19 2	Q84197 human respi
12	25	25.3	19 2	Q91329 human immun
13	25	25.3	19 2	Q9WMB1 human immun
14	25	25.3	20 1	P30900 equus asinus
15	25	25.3	20 2	Q9URC7 saccharomy
16	24.5	24.7	20 2	Q9R887 nitirospir
17	24.5	24.7	20 2	Q9RJA5 nitrosospir
18	24	24.2	11 2	Q5vbeB streptococc
19	24	24.2	11 2	AADG0518 streptococc
20	24	24.2	11 2	AADG0520 streptococc
21	24	24.2	11 2	AADG0522 streptococc
22	24	24.2	11 2	AADG0524 streptococc
23	24	24.2	11 2	AADG0526 streptococc
24	24	24.2	11 2	AadG0528 streptococc
25	24	24.2	11 2	AadG0530 streptococc
26	24	24.2	13 2	Q7TWW4 mus musculus
27	24	24.2	16 2	Q95557 bacillus sp
28	24	24.2	16 2	Q66737 equine infec
29	24	24.2	17 2	Q8IVK5 homo sapien
30	24	24.2	17 2	Q78381 human immun
31	24	24.2	18 2	Q9HBD6 homo sapien

105	21	21.2	14	2	06Q704	Q6q704	physocarpus	DR HSSP; P00342; 2LIX.
106	21	21.2	14	2	06Q706	Q6q706	physocarpus	FT NON_TER 1
107	21	21.2	14	2	06Q709	Q6q709	physocarpus	SEQUENCE 19 AA; 2203 MW;
108	21	21.2	14	2	06Q710	Q6q710	physocarpus	80D6B2E6F765516B CRC64;
109	21	21.2	14	2	06Q712	Q6q712	physocarpus	Query Match 30.3%; Score 30;
110	21	21.2	14	2	06Q713	Q6q713	vauquelina	DB 2; Length 19;
111	21	21.2	14	2	06Q714	Q6q714	lynothamnu	Best Local Similarity 71.4%;
112	21	21.2	14	2	AAS65671	Aas65671	lynotham	Score 30; Pred. 9.9e+02;
113	21	21.2	14	2	AAS65672	Aas65672	vauquelinia	Mismatches 1; Indels 0;
114	21	21.2	14	2	AAS65673	Aas65673	physocarp	Gaps 0;
115	21	21.2	14	2	AAS65674	Aas65674	physocarp	Db 6 SAU1LN 12
116	21	21.2	14	2	AAS65675	Aas65675	physocarp	
117	21	21.2	14	2	AAS65676	Aas65676	physocarp	
118	21	21.2	14	2	AAS65677	Aas65677	physocarp	
119	21	21.2	14	2	AAS65678	Aas65678	physocarp	
120	21	21.2	14	2	AAS65679	Aas65679	physocarp	
121	21	21.2	14	2	AAS65680	Aas65680	physocarp	
122	21	21.2	14	2	AAS65681	Aas65681	physocarp	
123	21	21.2	14	2	AAS65682	Aas65682	physocarp	
124	21	21.2	14	2	AAS65683	Aas65683	physocarp	
125	21	21.2	14	2	AAS65684	Aas65684	physocarp	
126	21	21.2	14	2	AAS65685	Aas65685	physocarp	
127	21	21.2	14	2	AAS65686	Aas65686	physocarp	
128	21	21.2	14	2	AAS65687	Aas65687	neillia a	
129	21	21.2	14	2	AAS65688	Aas65688	neillia s	
130	21	21.2	14	2	AAS65689	Aas65689	neillia s	
131	21	21.2	14	2	AAS65690	Aas65690	neillia s	
132	21	21.2	14	2	AAS65691	Aas65691	neillia t	
133	21	21.2	14	2	AAS65692	Aas65692	neillia t	
134	21	21.2	14	2	AAS65693	Aas65693	neillia t	
135	21	21.2	14	2	AAS65694	Aas65694	neillia t	
136	21	21.2	14	2	AAS65695	Aas65695	neillia t	
137	21	21.2	14	2	AAS65696	Aas65696	neillia u	
138	21	21.2	14	2	AAS65697	Aas65697	neillia u	
139	21	21.2	14	2	AAS65698	Aas65698	stephanian	
140	21	21.2	14	2	AAS65699	Aas65699	stephanian	
141	21	21.2	14	2	AAS6700	Aas6700	stephanian	
142	21	21.2	14	2	AAS6701	Aas6701	stephanian	
143	21	21.2	14	2	AAS6702	Aas6702	stephanian	
144	21	21.2	14	2	AAS6703	Aas6703	stephanian	
145	21	21.2	15	2	Q78007	Q78007	neurospora	Query Match 37.5%; Score 27.3%; DB 2; Length 20;
146	21	21.2	15	2	Q6LAG2	Q6LAG2	oryctolagus	Best Local Similarity 37.5%; Pred. No. 3.1e+03; Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
147	21	21.2	15	2	CAA77016	Ca97016	Ca97016	RNA-directed RNA polymerase activity; IEA.
148	21	21.2	17	2	Q62436	Q62436	mus musculus	KW RNA-dependent RNA polymerase.
149	21	21.2	17	2	Q9EP50	Q9EP50	unidentifie	FT Non_TER 20
150	21	21.2	18	1	TOP1_KLEAE	P46155	klebsiella	SQ SEQUENCE 20 AA; 2358 MW; 4F13BA084822ED09 CRC64;
<b>RESULT 1</b>								
ID Q62545	PRELIMINARY;	PRT;	19 AA.		Q8V86	Q8V86	PRELIMINARY;	PRT; 20 AA.
AC Q62545;	01-JUN-1998 (TREMBREL. 06, Created)	AC Q8V86;			AC Q8V86;		AC Q8V86;	
DT 01-JUN-1998 (TREMBREL. 06, Last sequence update)	DT 01-MAR-2002 (TREMBREL. 20, Last sequence update)	DT 01-MAR-2002 (TREMBREL. 20, Last sequence update)			DT 01-MAR-2002 (TREMBREL. 20, Last sequence update)		DT 01-MAR-2002 (TREMBREL. 20, Last sequence update)	
DT 01-JUN-2003 (TREMBREL. 24, Last annotation update)	DT 01-JUN-2003 (TREMBREL. 24, Last annotation update)	DT 01-JUN-2003 (TREMBREL. 24, Last annotation update)			DT 01-JUN-2003 (TREMBREL. 24, Last annotation update)		DT 01-JUN-2003 (TREMBREL. 24, Last annotation update)	
DE Lactate dehydrogenase-C (Fragment).					DE RNA-dependent RNA polymerase major subunit (Fragment).		DE RNA-dependent RNA polymerase major subunit (Fragment).	
OS Mus spretus (Western wild mouse).					OS Bovine respiratory syncytial virus (strain A5108) (BRSV).		OS Bovine respiratory syncytial virus (strain A5108) (BRSV).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;					OC Viruses; ssRNA negative-strand viruses; Mononegavirales;		OC Viruses; ssRNA negative-strand viruses; Mononegavirales;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					OC Paramyxoviridae; Pneumovirinae; Pneumovirus.		OC Paramyxoviridae; Pneumovirinae; Pneumovirus.	
OX NCBI_TaxID=10096;					OX NCBI_TaxID=11247;		OX NCBI_TaxID=11247;	
RP SEQUENCE FROM N.A.					RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	
RC STRAIN=SPPET/EI;					RC STRAIN=A51908;		RC STRAIN=A51908;	
RX MEDLINE=9431082; PubMed=8043949;					RX MEDLINE=21580793; PubMed=11724268;		RX MEDLINE=21580793; PubMed=11724268;	
RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,					RA Yunus A.S., Khattar S.K., Collins P.L., Samal S.K.;		RA Yunus A.S., Khattar S.K., Collins P.L., Samal S.K.;	
RA Nadeau J.H.;					RT "Rescue of bovine respiratory syncytial virus from cloned cDNA: entire		RT "Rescue of bovine respiratory syncytial virus from cloned cDNA: entire	
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";					RT genome sequence of BRSV strain A5108s;"		RT genome sequence of BRSV strain A5108s;"	
RL Mamn. Genome 5:349-355 (1994).					RL Virus Genes 23:157-164 (2001).		RL Virus Genes 23:157-164 (2001).	
DR EMBL; U05739; AAB60478-1; -.					DR EMBL; AY295544; AAL49413.1; -.		DR EMBL; AY295544; AAL49413.1; -.	
DR PIR; 149422; 149422.					DR PIR; PQ0300; PQ0300.		DR PIR; PQ0300; PQ0300.	
DR GO; GO:003968; RNA-directed RNA polymerase.					DR GO; GO:003968; RNA-directed RNA polymerase.		DR GO; GO:003968; RNA-directed RNA polymerase.	
DR NON_TER 20					DR NON_TER 20		DR NON_TER 20	
SQ SEQUENCE 20 AA; 2358 MW; 4F13BA084822ED09 CRC64;					SQ SEQUENCE 20 AA; 2358 MW; 4F13BA084822ED09 CRC64;		SQ SEQUENCE 20 AA; 2358 MW; 4F13BA084822ED09 CRC64;	

Query Match 27.3%; Score 27; DB 2; Length 20;  
Best Local Similarity 37.5%; Pred. No. 3.1e+03; Indels 0; Gaps 0;  
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 3 DGLWNNQNTQPLHNS 18  
Db 2 DTLIHENSTNWYLDS 17

**RESULT 4**

Q73378 PRELIMINARY; PRT; 17 AA.  
AC Q78378; ID Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Immunodeficiency virus type 1, viral sample FLPR5A (Florida patient  
DE B), partial env cds, VS region. (Fragment).  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OC NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-92271245; PubMed=1589795;  
RA Ou C.-Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,  
RA Korber B., T.M., Mullins J.I., Schuchterman G., Bertkelman R.L.,  
RA Economou A.N., Witte J.J., Satten G.A., Curran J.W.,  
RA Jaffe H.W.;  
RT "Molecular epidemiology of HIV transmission in a dental practice.";  
RL Science 256:1165-1171(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhang L.Q., Leigh-Brown A.J.;  
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.  
DR EMBL; MM2123; AAA44931; --.  
GO: GO:0019031; Cviral envelope; IEA.  
DR InterPro; IPR000777; GPI20.  
FT NON\_TER 1  
FT NON\_TER 17 17 MW; 34757935D12CA370 CRC64;  
SQ SEQUENCE 17 AA: 1723 MW; 34757935D12CA370 CRC64;

Query Match 26.3%; Score 26; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 3.8e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 NNNOTQLF 14  
Db 4 NTNEETFE 11

**RESULT 5**

Q9ETX8 PRELIMINARY; PRT; 19 AA.  
AC Q9ETX8;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Glutamate racemase (Fragment).  
GN Name=glr;  
OS Helicobacter pylori (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Gammaproteobacteria;  
OC Helicobacteraceae; Helicobacter.  
RN [1] - TaxID=210;  
RP SEQUENCE FROM N.A.

CR10, CR60, CR40, CR45, CR46, CR47, and CR39;  
RX MEDLINE-21117015; PubMed=1179371;  
RA Occhialini A., Marais A., Urdaci M., Sierra R., Munoz N., Covacci A.,  
RA Megraud F.;  
RT "Composition and gene expression of the cag pathogenicity island in  
RT Helicobacter pylori strains isolated from gastric carcinoma and  
RT gastritis patients in Costa Rica.";  
RL Infect. Immun. 69:1902-1908 (2001).

Query Match 26.3%; Score 26; DB 2; Length 19;  
Best Local Similarity 31.2%; Pred. No. 4.3e+03; Indels 0; Gaps 0;  
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SSDGLWNNQNTQPLE 16  
Db 3 SGDVIWLEKQAKEWLK 18

**RESULT 6**

Q6SY5 PRELIMINARY; PRT; 20 AA.  
AC Q6SY5;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DE Epidermal growth factor receptor (Fragment).  
GN Name=EGFR; ORNames=CG10079;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephyrdoidea; Drosophilidae; Drosophila.  
RN NCBI\_TaxID=7227;  
RP SEQUENCE FROM N.A.  
RC STRAIN=CA098;  
RA Palsson A., Rouse A., Riley-Berger R., Dworkin I., Gibson G.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AV46079; AAB84726; 1;  
GO: GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2332 MW; E3AC72FPBBP98357 CRC64;

Query Match 26.3%; Score 26; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 4.5e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SDGLWNN 9  
Db 11 SRGLWDSS 18

**RESULT 7**

A0R04726 PRELIMINARY; PRT; 20 AA.  
ID A0R04726  
AC AAB84726;  
DT 02-MAR-2004 (Tremblrel. 27, Created)  
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)  
DE Epidermal growth factor receptor (Fragment).  
GN EGFR OR CG10079;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephyrdoidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CA098;  
RA Palsson A., Rouse A., Riley-Berger R., Dworkin I., Gibson G.;  
RA Palsson A., Rouse A., Riley-Berger R., Dworkin I., Gibson G.;  
RT "Nucleotide variation in the EGFR locus of Drosophila melanogaster.";  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

DR	EMBL;	AY460749;	AAR84726.1;	-.
KW	Receptor.	20	20	
FT	NON_TER	20 AA;	2332 MW;	E3ACT2F1BBFF9E357 CRC64;
SQ	SBOJENCE	20 AA;		
Qy	2	SDGJWNNN 9		
Db	11	SRGLWDSS 18		
RESULT 8				
ID	Q9TR47	PRELIMINARY;	PRT;	10 AA.
AC	Q9TR47;			
DT	01-MAY-2000	(TREMBrel. 13, Last sequence update)		
DE	01-DEC-2001	(TREMBrel. 19, Last annotation update)		
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccora; Bovidae;			
OC	Bovinae; Bos;			
RX	NCBI_TaxID=9913;			
RP	SEQUENCE.			
[1]	Nagashima M., Lund B.R., Vijay S., Nitecki D., Zhang J., Chen J.X., Hori O., Brett J., Slatter T., Gao R., "The receptor for advanced glycation end products (RAGE) is a cellular binding site for amphotericin. Mediation of neurite outgrowth and co-expression of rage and amphotericin in the developing nervous system.", J. Biol. Chem. 270: 25752-25761(1995).			
SQ	SEQUENCE 10 AA; 1163 MW; 28E03443769B18 CRC64;			
Query Match	25.3%; Score 25; DB 2; Length 10;			
Best Local Similarity	75.0%; Pred. No. 3e+03;			
Matches	3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
Qy	5 LWNN 8			
Db	5 MWNN 8			
RESULT 9				
ID	Q15610	PRELIMINARY;	PRT;	19 AA.
AC	Q15610;			
DT	01-NOV-1996	(TREMBrel. 01, Created)		
DT	01-JUL-1997	(TREMBrel. 04, Last sequence update)		
DT	01-JUN-2003	(TREMBrel. 24, Last annotation update)		
DE	Topoisomerase I (Fragment), Name=TOP1;			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	[1] SEQUENCE FROM N.A.			
RP	MEDLINE:91093302; PubMed=2176592;			
RX	Kunze N., Klein M., Richter A., Knippers R.; "Structural characterisation of the human DNA topoisomerase I gene promoter.", Eur. J. Biochem. 194: 323-330(1990).			
RX	DR: GO:0016853; F-isomerase activity; IEA.			
RX	KW 1-bomerase.			
SEQUENCE	19 AA; 2236 MW; 47DBD36F44FFEEFB CRC64;			
Query Match	25.3%; Score 25; DB 2; Length 19;			
Best Local Similarity	31.2%; Pred. No. 6.1e+03; Mismatches 8; Indels 0; Gaps 0;			
Matches	4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;			
Qy	1 SSDGLUNNNNQQLPF 14			
Db	2 SGDHLINDSQQFFF 15			
RESULT 10				
ID	Q9ETX7	PRELIMINARY;	PRT;	19 AA.
AC	Q9ETX7;			
DT	01-MAR-2001	(TREMBrel. 16, Last sequence update)		
DT	01-MAR-2001	(TREMBrel. 16, Last annotation update)		
DE	Glutamate racemase (Fragment).			
GN	Name=GLR;			
OS	Helicobacter pylori (Campylobacter pylori).			
OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;			
OC	Helicobacteraceae; Helicobacter.			
OX	NCBI_TaxID=210;			
RN	[1] SEQUENCE FROM N.A.			
RP	STRAIN=CR41, and CR44;			
RX	MEDLINE=2117015; PubMed=1179371;			
RA	Occhialini A., Marais A., Uracci M., Sierra R., Munoz N., Covacci A., Megraud F.; "Composition and gene expression of the cag pathogenicity island in Helicobacter pylori strains isolated from gastric carcinoma and gastritis patients from Costa Rica.", Infect. Immun. 69: 1902-1908(2001).			
RT	"Composition and gene expression of the cag pathogenicity island in Helicobacter pylori strains isolated from gastric carcinoma and gastritis patients from Costa Rica.", Infect. Immun. 69: 1902-1908(2001).			
RL	DR: EMBL; AF289398; AAG09846.1; -.			
DR	EMBL; AF289392; AAG09834.1; -.			
FT	NON_TER 1 1			
SQ	SEQUENCE 19 AA; 2238 MW; 6FF0977B72DFE7C5 CRC64;			
Query Match	25.3%; Score 25; DB 2; Length 19;			
Best Local Similarity	31.2%; Pred. No. 6.1e+03; Mismatches 7; Indels 0; Gaps 0;			
Matches	5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;			
Qy	1 SSDGLUNNNNQQLPF 16			
Db	3 SGDVVVLEKQAKEWLK 18			
RESULT 11				
ID	Q84197	PRELIMINARY;	PRT;	19 AA.
AC	Q84197;			
DT	01-NOV-1996	(TREMBrel. 01, Created)		
DT	01-NOV-1996	(TREMBrel. 01, Last sequence update)		
DT	01-JAN-1999	(TREMBrel. 09, Last annotation update)		
DE	L protein (Fragment).			
OS	Human respiratory syncytial virus (subgroup B / strain 18537).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;			
OC	Paronyxoviridae; Pneumovirinae; Pneumovirus;			
OC	Human respiratory syncytial virus B.			
OX	NCBI_TaxID=11251;			
RN	[1] SEQUENCE FROM N.A.			
RP	MEDLINE=8036169; PubMed=3183631;			
RX	Johnson P.R., Collins P.L.; "The A and B subgroups of human respiratory syncytial virus: Comparison of intergenic and gene-overlap sequences.", J. Gen. Virol. 69: 2901-2906(1988).			
RT	"The A and B subgroups of human respiratory syncytial virus: Comparison of intergenic and gene-overlap sequences.", J. Gen. Virol. 69: 2901-2906(1988).			
RL	DR: EMBL; D00397; BAR2058.1; -.			
DR	EMBL; D00397; BAR2058.1; -.			
SQ	SEQUENCE 19 AA; 2100 MW; 8277C94820609735 CRC64;			
Query Match	25.3%; Score 25; DB 2; Length 19;			
Best Local Similarity	31.2%; Pred. No. 6.1e+03; Mismatches 8; Indels 0; Gaps 0;			
Matches	4; Conservative 3; Mismatches 8; Indels 0; Gaps 0;			
Qy	1    ::: 1			
Db	2 SGDHLINDSQQFFF 15			

Qy	3 DGLWNNNOTOFLEHS 18	KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
Db	2 DPINGNSANVLTDS 17	FT NON_TER 1 1
		SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
		SQ
RESULT 12		Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
091329	PRELIMINARY; PRT; 19 AA.	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
ID		RP
AC	091329;	NON_TER 1
DT	01-NOV-1998 (TREMBLrel. 08, Created)	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)	SQ
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
GT		Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB	Envelope glycoprotein (Fragment).	RP
OS	Human immunodeficiency virus 1.	NON_TER 1
OC	Viruses; Retroviridae; Lentivirus.	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
GN	Namesenv; NCBITaxID:1176;	SQ
OX		Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
RN	[1] SEQUENCE FROM N.A.	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RP		RP
RX	MEDLINE=98285741; PubMed=9621043;	NON_TER 1
RA	Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
RA	Safar M., Barre-Sinoussi F., Kazatchkine M.D.,	SQ
RT	"Genetically related human immunodeficiency virus type 1 in three adults of a family with no identified risk factor for intrafamilial transmission.";	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
RT	J. Virol. 72:5831-5839(1998).	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DR	EMBL: U87220; AAC32980.;	RP
DR	GO; GO:0019028; C:viral capsid; IEA.	NON_TER 1
DR	GO; GO:0019031; C:viral envelope; IEA.	SEQUENCE : 19 AA; 2294 MW; 379CB14A9B073911 CRC64;
DR	GO; GO:0005198; F:structural molecule activity; IEA.	SQ
DR	InterPro; IPR000777; GP120.	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
DR	PFAM; PF00516; GP120.;	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
KW	AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.	RP
FT	NON_TER 1	NON_TER 1
FT	NON_TER 1	SEQUENCE : 19 AA; 2294 MW; 379CB14A9B073911 CRC64;
FT	NON_TER 1	SQ
QT	SEQUENCE FROM N.A.	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
RP		Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RX	MEDLINE=98285741; PubMed=9621043;	RP
RA	Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,	NON_TER 1
RA	Safar M., Barre-Sinoussi F., Kazatchkine M.D.,	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
RT	"Genetically related human immunodeficiency virus type 1 in three adults of a family with no identified risk factor for intrafamilial transmission.";	SQ
RT	J. Virol. 72:5831-5839(1998).	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
DR	EMBL: U87220; AAC32976.1.;	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DR	GO; GO:0019028; C:viral capsid; IEA.	RP
DR	GO; GO:0019031; C:viral envelope; IEA.	NON_TER 1
DR	GO; GO:0005198; F:structural molecule activity; IEA.	SEQUENCE : 19 AA; 2294 MW; 379CB14A9B073911 CRC64;
DR	InterPro; IPR000777; GP120.	SQ
DR	PFAM; PF00516; GP120.;	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
DR	GO; GO:0003745; F:translation elongation factor activity; IEA.	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULT 14		RP
ALBG_EQUAS	PRELIMINARY; PRT; 20 AA.	NON_TER 1
ID	ALBG_EQUAS	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
AC	P39090;	SQ
DT	01-FEB-1995 (Rel. 31, Created)	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
DT	05-JUL-2004 (Rel. 44, Last annotation update)	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DE	Alpha-1B-glycoprotein (Alpha-1B glycoprotein) (Postalbumin) (Fragment).	RP
GN	Name=ALBG;	NON_TER 1
OS	Equus asinus (Donkey)	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.	SQ
OC	NCBI_TaxID:9793;	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
RN	[1]	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RP	SEQUENCE.	RP
RC	TISSUE=Plasma;	NON_TER 1
RX	MEDLINE=91330579; PubMed=1868686;	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
RA	Patterson S.D., Bell K., Shaw D.C.;	SQ
RA	"Donkey and horse alpha 1-B-glycoprotein: partial characterization and new alleles."	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
RT	PFAM; PF00516; GP120.;	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RL	Comp. Biochem. Physiol. 98B:523-528 (1991).	RP
CC	-1- FUNCTION: Unknown.	NON_TER 1
CC	-1- SUBCELLULAR LOCATION: Secreted.	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
CC	-1- TISSUE SPECIFICITY: Plasma.	SQ
CC	Direct protein sequencing; Glycoprotein; Immunoglobulin domain; Plasma.	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 20;
KW	Plasma.	Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
FT	NON_TER 1	RP
FT	NON_TER 1	SEQUENCE : 20 AA; 2197 MW; 65857DFD468EBDPF CRC64;
QT	SEQUENCE	SQ
Qy	5 IWNNNNOTQL 13	Query Match Best Local Similarity 25.3%; Score 25; DB 1; Length 20;
Db	10 LWAADTQL 18	Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
RESULT 15		RP
Q9URC7	PRELIMINARY; PRT; 20 AA.	NON_TER 1
ID	Q9URC7	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
AC	Q9URC7;	SQ
DT	01-MAY-2000 (TREMBLrel. 13, Created)	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	RP
DB	Lipid-binding protein (Fragment).	NON_TER 1
OS	Saccharomyces cerevisiae (Baker's yeast).	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
OC	Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetidae; Saccharomycetaceae; Saccharomyces.	SQ
OC	NCBI_TaxID:4932;	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
RN	[1]	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RP	SEQUENCE.	RP
RX	MEDLINE=91353077; PubMed=18682548;	NON_TER 1
RA	Crautz C.B., Snyder S.L., Kambouris N.G.;	SEQUENCE : 19 AA; 2294 MW; 3781714A9B073911 CRC64;
RA	"Calcium-dependent secretory vesicle-binding and lipid-binding proteins of Saccharomyces cerevisiae."	SQ
RT	Yeast 7:229-244 (1991).	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
RT	PFAM; PF00516; GP120.;	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DR	GO; GO:0003745; F:translation elongation factor activity; IEA.	RP
DR	InterPro; IPR000777; GP120.	NON_TER 1
DR	PFAM; PF00516; GP120.;	Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;
DR	GO; GO:0003745; F:translation elongation factor activity; IEA.	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DR	GO; GO:0006414; P:translational elongation; IEA.
DR	InterPro; IPR01326; EBI1.BD.
PFAM	Pfam; Q9P36; EBI1.GNB; T.
FT	NON_TER
FT	NON_TER
SQ	SEQUENCE 20 AA; 2388 MW; 594377CBC3E7B0D CRC64;
QY	Query Match 25.3%; Score 25; DB 2; Length 20; Best Local Similarity 37.5%; Pred. No. 6.5e+03; Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
DB	6 WNNNOTOL 13  :::  5 WDDDETLN 12
RESULT 16	
ID	Q9R987 PRELIMINARY; PRT; 20 AA.
ID	Q9R987_01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Ammonia monooxygenase subunit C1 (Fragment).
GN	Name-amOC1;
OS	Nitrosospira sp. NP39-19.
OC	Bacteria; Proteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosospira.
OC	NCBI_TaxID=61907;
RP	SEQUENCE FROM N.A.
RC	STRAIN=NP39-19;
RX	MEDLINE=21665709; PubMed=11807563;
RA	Norton J.M., Alvarez J.J., Suwa Y., Klotz M.G.; "Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria," Arch. Microbiol. 177:139-149(2002).
RA	Norton J.M., Alvarez J.J., Suwa Y., Klotz M.G.; "Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria," Arch. Microbiol. 177:139-149(2002).
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NP39-19;
RX	MEDLINE=91306641; PubMed=9163908;
RA	Klotz M.G., Alvarez J.J., Norton J.M.; "A gene encoding a membrane protein exists upstream of the amoA/amoB genes in ammonia oxidizing bacteria: a third member of the amo operon?"; FEMS Microbiol. Lett. 150:65-73(1997).
RL	[4]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NP39-19;
RX	MEDLINE=21665709; PubMed=11807563;
RA	Norton J.M., Alvarez J.J., Suwa Y., Klotz M.G.; "Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria," Arch. Microbiol. 177:139-149(2002).
RA	EMBL; AF032438; AAB6880.1; -.
DR	GO; GO:0004497; P:monooxygenase activity; IEA.
DR	GO; GO:0004497; P:monooxygenase activity; IEA.
RT	"Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria," Arch. Microbiol. 177:139-149(2002).
RL	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NP39-19;
RA	Shiozawa T.L., Norton J.M., Alvarez J.J., Klotz M.G.; EMBL; AF042170; AAC25054.1; -.
DR	GO; GO:0004497; P:monooxygenase activity; IEA.
KW	Monooxygenase.
FT	NON_TER 1 1
SQ	SEQUENCE 20 AA; 2266 MW; A745DC66ACC3F2A9 CRC64;
QY	Query Match 24.7%; Score 24.5; DB 2; Length 20; Best Local Similarity 31.2%; Pred. No. 7.8e+03; Matches 5; Conservative 6; Mismatches 4; Indels 1; Gaps 1;
DB	2 SDGLWNNNOTQFLEH 17 2 TDVW-NGQSKVILNN 16
RESULT 17	
ID	Q9YB88 PRELIMINARY; PRT; 11 AA.
ID	Q9YB88_01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Ammonia monooxygenase 1 subunit C (Fragment).
GN	Name-amOC1;
OS	Nitrosospira sp. NP4V.
OC	Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosospira.
OC	NCBI_TaxID=58133;
QY	2 SDGLWNNNOTQFLEH 17 2 TDVW-NGQSKVILNN 16
DB	2 TDVW-NGQSKVILNN 16
RESULT 18	
ID	Q9YB88 PRELIMINARY; PRT; 11 AA.
ID	Q9YB88_05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	Wzx (Fragment).
GN	Name-wzx;
OS	Streptococcus pneumoniae.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
OC	NCBI_TaxID=1313;
QY	1
DB	SEQUENCE FROM N.A.
RC	STRAIN=MA053392; NZSPN00/319, NZSPN01/278, MA050663, MA052628, 015009, and MA062510; MEDLINE=22997121; PubMed=14614062;
RA	Kong F., Gilbert G.;
RT	"Using cpa-cpsB sequence polymorphisms and serotype-/group-specific PCR to predict 51 Streptococcus pneumoniae capsular serotypes," J. Med. Microbiol. 52:1047-1058 (2003).
RT	EMBL; AY163227; AAO0520.1; -.
DR	EMBL; AY163228; AAO0522.1; -.
DR	EMBL; AY163229; AAO0524.1; -.
DR	EMBL; AY163230; AAO0526.1; -.
DR	EMBL; AY163231; AAO0528.1; -.
DR	EMBL; AY163232; AAO0530.1; -.
RP	SEQUENCE FROM N.A.
RC	STRAIN=NPAV;

	DR	EMBL; AY163226; AAO60518.1; -.
	FT	NON_TER
	SQ	SEQUENCE 11 AA; 1456 MW; EEB6B29E7C721F1A1 CRC64;
Query Match	Best Local Similarity 24.2%; Score 24; DB 2; Length 11; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	14 FLEHS 18	
Db	1 FLEHT 5	
RESULT 19		
ID	AA060518	PRELIMINARY; PRT; 11 AA.
AC	AA060518;	
DT	02-MAR-2004	(TREMBLrel. 27, Last sequence update)
DT	02-MAR-2004	(TREMBLrel. 27, Last annotation update)
DE	Wzx (Fragment).	
GN	Wzx.	
OS	Streptococcus pneumoniae.	
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
RX	NCBI_TaxID=1313;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=MA062610;	
RC	MEDLINE=22979121; PubMed=14614062;	
RA	Kong F., Gilbert G.L.,	"Using cbsA-csbB sequence polymorphisms and serotype-/group-specific PCR to predict 51 streptococcus pneumoniae capsular serotypes.";
RT	J. Med. Microbiol. 52:1047-1058 (2003).	
RL	J. Med. Microbiol. 52:1047-1058 (2003).	
DR	EMBL; AY163226; AAO60518.1; -.	
FT	NON_TER 1	
SQ	SEQUENCE 11 AA; 1456 MW; EEB6B29E7C721F1A1 CRC64;	
Query Match	Best Local Similarity 80.0%; Pred. No. 4.8e+03; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	14 FLEHS 18	
Db	1 FLEHT 5	
RESULT 20		
ID	AA060520	PRELIMINARY; PRT; 11 AA.
AC	AA060520;	
DT	02-MAR-2004	(TREMBLrel. 27, Created)
DT	02-MAR-2004	(TREMBLrel. 27, Last sequence update)
DT	02-MAR-2004	(TREMBLrel. 27, Last annotation update)
DE	Wzx (Fragment).	
GN	Wzx.	
OS	Streptococcus pneumoniae.	
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=MA05332;	
RC	MEDLINE=22979121; PubMed=14614062;	
RA	Kong F., Gilbert G.L.,	"Using cbsA-csbB sequence polymorphisms and serotype-/group-specific PCR to predict 51 streptococcus pneumoniae capsular serotypes.";
RT	J. Med. Microbiol. 52:1047-1058 (2003).	
RL	J. Med. Microbiol. 52:1047-1058 (2003).	
DR	EMBL; AY163227; AAO60520.1; -.	
FT	NON_TER 1	
SQ	SEQUENCE 11 AA; 1456 MW; EEB6B29E7C721F1A1 CRC64;	
Query Match	Best Local Similarity 80.0%; Pred. No. 4.8e+03; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	14 FLEHS 18	
Db	1 FLEHT 5	
RESULT 21		
ID	AA060522	PRELIMINARY; PRT; 11 AA.
AC	AA060522;	
DT	02-MAR-2004	(TREMBLrel. 27, Created)
DT	02-MAR-2004	(TREMBLrel. 27, Last sequence update)
DE	Wzx (Fragment).	
GN	Wzx.	
OS	Streptococcus pneumoniae.	
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
RX	NCBI_TaxID=1313;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=NASPN01/278;	
RC	MEDLINE=22979121; PubMed=14614062;	
RA	Kong F., Gilbert G.L.,	"Using cbsA-csbB sequence polymorphisms and serotype-/group-specific PCR to predict 51 streptococcus pneumoniae capsular serotypes.";
RT	J. Med. Microbiol. 52:1047-1058 (2003).	
RL	J. Med. Microbiol. 52:1047-1058 (2003).	
DR	EMBL; AY163229; AAO60524.1; -.	
FT	NON_TER 1	
SQ	SEQUENCE 11 AA; 1456 MW; EEB6B29E7C721F1A1 CRC64;	
Query Match	Best Local Similarity 80.0%; Pred. No. 4.8e+03; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	14 FLEHS 18	
Db	1 FLEHT 5	

Db	1 FLEHT 5	PRELIMINARY;	PRT;	11 AA.
RESULT 23				
ID AAO60526	PRELIMINARY;	PRT;	11 AA.	
AC AAO60526;				
DT 02-MAR-2004 (TREMBrel. 27, Created)				
DT 02-MAR-2004 (TREMBrel. 27, Last sequence update)				
DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)				
DE WZX (Fragment).				
GN				
OS Streptococcus pneumoniae.				
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC Streptococcus;				
OX NCBI_TAXID=1313;				
RN [1]				
SEQUENCE FROM N.A.				
RC STRAIN=MA050663;				
RX MEDLINE=22979121; PubMed=14614062;				
RA Kong F.; Gilbert G. I.;				
RT "Using cPSA-cPSB sequence polymorphisms and serotype-/group-specific				
RT PCR to predict S1 Streptococcus pneumoniae capsular serotypes.";				
RL J. Med. Microbiol. 52:1047-1058 (2003).				
DR EMBL; AY163230; AAO60526.1; -.				
FT NON_TER	1			
SQ SEQUENCE 11 AA; 1456 MW; EE6B29E7C721F1A1 CRC64;				
Query Match 24.2%; Score 24; DB 2; Length 11;				
Best Local Similarity 80.0%; Pred. No. 4.8e+03;				
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY 14 FLEHS 18				
Db 1 FLEHT 5				
RESULT 24				
ID AAO60528	PRELIMINARY;	PRT;	11 AA.	
AC AAO60528;				
DT 02-MAR-2004 (TREMBrel. 27, Created)				
DT 02-MAR-2004 (TREMBrel. 27, Last sequence update)				
DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)				
DE WZX (Fragment).				
GN				
OS Streptococcus pneumoniae.				
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC Streptococcus;				
OX NCBI_TAXID=1313;				
RN [1]				
SEQUENCE FROM N.A.				
RC STRAIN=MA050663;				
RX MEDLINE=22979121; PubMed=14614062;				
RA Kong F.; Gilbert G. I.;				
RT "Using cPSA-cPSB sequence polymorphisms and serotype-/group-specific				
RT PCR to predict S1 Streptococcus pneumoniae capsular serotypes.";				
RL J. Med. Microbiol. 52:1047-1058 (2003).				
DR EMBL; AY163231; AAO60528.1; -.				
FT NON_TER	1			
SQ SEQUENCE 11 AA; 1456 MW; EE6B29E7C721F1A1 CRC64;				
Query Match 24.2%; Score 24; DB 2; Length 11;				
Best Local Similarity 80.0%; Pred. No. 4.8e+03;				
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY 14 FLEHS 18				
Db 1 FLEHT 5				
RESULT 25				
ID AAO60530	PRELIMINARY;	PRT;	11 AA.	
AC AAO60530;				
DT 02-MAR-2004 (TREMBrel. 27, Created)				
DT 02-MAR-2004 (TREMBrel. 27, Last sequence update)				
DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)				
DE WZX (Fragment).				
GN				
OS Streptococcus pneumoniae.				
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC Streptococcus;				
OX NCBI_TAXID=1313;				
RN [1]				
SEQUENCE FROM N.A.				
RC STRAIN=MA050663;				
RX MEDLINE=22979121; PubMed=14614062;				
RA Kong F.; Gilbert G. I.;				
RT "Using cPSA-cPSB sequence polymorphisms and serotype-/group-specific				
RT PCR to predict S1 Streptococcus pneumoniae capsular serotypes.";				
RL J. Med. Microbiol. 52:1047-1058 (2003).				
DR EMBL; AY163231; AAO60528.1; -.				
FT NON_TER	1			
SQ SEQUENCE 11 AA; 1456 MW; EE6B29E7C721F1A1 CRC64;				
Query Match 24.2%; Score 24; DB 2; Length 11;				
Best Local Similarity 80.0%; Pred. No. 4.8e+03;				
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY 14 FLEHS 18				
Db 1 FLEHT 5				
RESULT 26				
ID Q7TM4	PRELIMINARY;	PRT;	13 AA.	
AC Q7TM4				
DT 01-OCT-2003 (TREMBrel. 25, Created)				
DT 05-JUL-2004 (TREMBrel. 25, Last sequence update)				
DE UORP4 (TDRP2).				
GN Name=ElF5a;				
OS Mus musculus (Mouse).				
OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX NCBI_TAXID=10090;				
RN [1]				
SEQUENCE FROM N.A.				
RC STRAIN=BALB/c;				
RA Jenkins Z.A.; Johansson H.E.;				
RT Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.				
DR EMBL; AY129344; AAN17555.1; -.				
DR EMBL; AY129346; AAN17530.1; -.				
DR EMBL; AY129329; AAN17537.1; -.				
DR GO; GO:0005737; Cyttoplasm; IDA.				
DR GO; GO:0005634; Cytoplasm; IDA.				
DR GO; GO:0006915; Papoplosis; IDA.				
DR GO; GO:0006915; Papoplosis; IDA.				
SQ SEQUENCE 13 AA; 1477 MW; 8AAH04CCP18E35A5 CRC64;				
Query Match 24.2%; Score 24; DB 2; Length 13;				
Best Local Similarity 50.0%; Pred. No. 5.8e+03;				
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
QY 4 GLMWN 9				
Db 2 GLWSS 7				
RESULT 27				
ID Q9R557	PRELIMINARY;	PRT;	16 AA.	
AC Q9R557				
DT 01-MAY-2000 (TREMBrel. 13, Created)				
DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)				
DR AAO60530				

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Subtilisin GX (Fragment).  
OS *Bacillus* sp.  
OC *Bacteria*; *Firmicutes*; *Bacillales*; *Bacillaceae*; *Bacillus*.  
OX NCBI\_TaxID=1409;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE:93356814; PubMed=8352796;  
RA Durham D.R.;  
RT "The electrolytic properties of subtilisin GX from alkalophilic  
*Bacillus* sp. strain 6644 provides a means of differentiation from  
other subtilins".  
RL Biochem. Biophys. Res. Commun. 194:1365-1370(1993).  
DR PIR; PC1299; PC1299;  
SQ SEQUENCE 16 AA; 1804 MW; 000FB22FEB9940C94 CRC64;

Query Match 24.2%; Score 24; DB 2; Length 16;  
Best local Similarity 42.9%; Pred. No. 7.3e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 2; Mismatches 2; Qy 6 WNNNOTQ 12  
Db 5 WGDNRVO 11

RESULT 28  
ID 066737 PRELIMINARY; PRT; 16 AA.  
AC 066737;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DB Transmembrane protein (Fragment).  
OS Equine infectious anemia virus.  
OC Viruses; Retrovirus; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN="Wyoming wild type non-cell culture adapted; TISSUE=Blood;  
RX MEDLINE:9229230; PubMed=1318398;  
RA Perry S.T.; Flaherty M.M.; Kelley M.J.; Clabough D.L.; Tronick S.R.,  
Coggin L.; Whetter L.; Lengel C.R.; Fuller F.J.;  
RT "The surface envelope protein gene region of equine infectious anemia  
virus is not an important determinant of tropism in vitro.";  
RL J. Virol. 66:4085-4097(1992).  
DR EMBL; MB7589; AAA10311;  
DR GO; GO:00116021; C:viral capsid; IEA.  
DR GO; GO:0005188; F:structural molecule activity; IEA.  
DR InterPro; IPR01367; Gp0\_EIAV.  
DR Pfam; PF00971; EIAV\_GP30; 1.  
KW Transmembrane.  
FT NON\_TER 16 16 16 AA; 1918 MW; BAE09AF8B99A3DB4 CRC64;  
SQ SEQUENCE 16 AA; 1918 MW; BAE09AF8B99A3DB4 CRC64;

Query Match 24.2%; Score 24; DB 2; Length 16;  
Best local Similarity 66.7%; Pred. No. 7.3e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Qy 8 NNQTOQ 13  
Db 9 NNKITBL 14

RESULT 29  
ID Q8YIK5 PRELIMINARY; PRT; 17 AA.  
AC Q8YIK5;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Stearin2 protein (Fragment).  
GN Name=STEERIN2;

RESULT 30  
ID Q78381 PRELIMINARY; PRT; 17 AA.  
AC Q78381;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DB Immunodeficiency virus type 1, viral sample FLIPRSF (Florida patient  
B), partial env cds, V5 region. (Fragment).  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirus; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:92271245; PubMed=1599796;  
RA Ou C.-Y.; Ciepielowski C.A.; Myers G.; Bandea C.I.; Luo C.C.,  
RA Korber B.T.M.; Mullins J.I.; Schatzlein G.; Beekelman R.L.,  
RA Economou A.N.; Witte J.J.; Furman L.J.; Satten G.A.; Curran J.W.,  
RA Jaffe H.W.;  
RT "Molecular epidemiology of HIV transmission in a dental practice.";  
RL Science 256:1165-1171(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhang L.Q.; Leigh-Brown A.J.;  
RL Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; M93126; AAA44961;  
DR GO; GO:00119031; C:viral envelope; IEA.  
DR InterPro; IPR000777; GPI20.  
FT NON\_TER 17 17 17 AA; 1708 MW; 347570D2D12CA370 CRC64;  
SQ SEQUENCE 17 AA; 1708 MW; 347570D2D12CA370 CRC64;

Query Match 24.2%; Score 24; DB 2; Length 17;  
Best local Similarity 50.0%; Pred. No. 7.8e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0; Qy 7 NNQTOQF 14  
Db 4 NTNNTETF 11

RESULT 31  
ID Q9HBD6 PRELIMINARY; PRT; 18 AA.  
AC Q9HBD6;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE ATPB (Fragment).  
GN Name=ATPB;  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 RN NCBI\_TaxID=9606;  
 [1] SEQUENCE FROM N.A.  
 RA Wang N., Wu Z.Y., Murong S.X., Lin M.T., Fang L.;  
 RT "hot point mutations of Wilson disease gene in Chinese with DNA  
 sequencing.";  
 RL Chung-Hua Shen Ching Ko Tsa Chih 31:20-23(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Wu Z.Y., Wang N., Murong S.X.;  
 RL Submitted (ABR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AR254565; AAG27522.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 18 AA; 2100 MW; B9E7PA2B#70B0378 CRC64;  
 Query Match 24.2%; Score 24; DB 2; Length 18;  
 Best Local Similarity 42.9%; Pred. No. 8.3e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 8; Gaps 1;  
 QY 4 GLWNNNQNOTLPLEH 17  
 Db 13 GLW-----LEH 18  
 RESULT 32  
 ID Q9ZG65 PRELIMINARY; PRT; 18 AA.  
 AC Q9ZG65;  
 DT 01-MAY-1999 (TREMBREL\_10, Created)  
 DT 01-MAY-1999 (TREMBREL\_10, Last sequence update)  
 DE Orotidine-5'-phosphate decarboxylase (Fragment).  
 GN Name=pYFR;  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OC NCBI\_TaxID=813;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=L2 434B;  
 RA Wang L., Steenberg S.D., Zheng Y., Larsen S.H.;  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF008729.1; AA004068.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 18 AA; 2026 MW; CB911767583AF4B3 CRC64;  
 Query Match 24.2%; Score 24; DB 2; Length 18;  
 Best Local Similarity 36.4%; Pred. No. 8.3e+03;  
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 SDSGIWNNNOT 11  
 Db 2 SSETSWNTRNS 12  
 RESULT 33  
 ID Q9QH4 PRELIMINARY; PRT; 19 AA.  
 AC Q9QH4;  
 DT 01-MAY-2000 (TREMBREL\_13, Created)  
 DT 01-MAY-2000 (TREMBREL\_13, Last sequence update)  
 DE Oligodendrocyte-specific UDP-Galactose:ceramide galactosyltransferase  
 (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Leukemia;  
 RX MEDLINE=96085162; PubMed=8521863;  
 RA Schulte S., Stoffel W.;  
 RT "UNG galactosidase:ceramide galactosyltransferase and glutamate/aspartate  
 transporter. Copurification, separation and characterization of the  
 two glycoproteins.";  
 RL Eur. J. Biochem. 233:947-953 (1995).  
 SQ SEQUENCE 19 AA; 1995 MW; 0FD4BAR3503B#9454 CRC64;  
 Query Match 24.2%; Score 24; DB 2; Length 19;  
 Best Local Similarity 80.0%; Pred. No. 8.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 SDGLW 6  
 Db 5 STGLW 9  
 RESULT 34  
 ID Q9QV32 PRELIMINARY; PRT; 19 AA.  
 AC Q9QV32;  
 DT 01-MAY-2000 (TREMBREL\_13, Created)  
 DT 01-MAY-2000 (TREMBREL\_13, Last sequence update)  
 DT 01-JUN-2002 (TREMBREL\_21, Last annotation update)  
 DE G3.5 ANTI-GEN-ALPHA-actinin (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE.  
 RA Price K.A., Malhotra S.K., Koke J.R.;  
 RT "Localization and characterization of an intermediate filament-  
 associated protein.";  
 RL Submitted (KXX-1993) to the EMBL/GenBank/DBJ databases.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 19 AA; 2205 MW; 505724CB038EB#879 CRC64;  
 Query Match 24.2%; Score 24; DB 2; Length 19;  
 Best Local Similarity 40.0%; Pred. No. 8.8e+03;  
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 NNQNOTLPLEH 17  
 Db 7 NLAMQIFPVKH 16  
 RESULT 35  
 ID LP#3\_HUMAN STANDARD; PRT; 20 AA.  
 AC P5643;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update) (Fragment).  
 DE Lysophospholipase HL-60 peak 3 (EC 3.1.1.5).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Leukemia;  
 RX MEDLINE=93111958; PubMed=17171998;  
 RA Garsett D., Hollenberg F., Steiner M.R., Egan R.W., Clark M.A.,  
 RT "Butyric acid-induced differentiation of HL-60 cells increases the  
 expression of a single lysophospholipase.";  
 RL Biochem. J. 288:831-837 (1992).  
 CC -I FUNCTION: Degradation of lysophospholipids.  
 CC -I CATALYTIC ACTIVITY: 2'-lysophosphatidylcholine + H(2)O =  
 CC glycerophosphocholine + a fatty acid anion.  
 CC -I PTM: The N terminus is blocked.  
 PIR; S27351; S27351.

DR GO; GO:0004622; **P**lybosphopholipase activity; IDA.  
 DR GO; GO:0009395; **P**hospholipid catabolism; NAS.  
 KW Direct protein sequencing; Hydrolase; Lipid degradation.  
 FT NON\_TER 1 1  
 SEQUENCE 20 AA; 2263 MW; 4D298E6D3F21F87F CRC64;  
 Query Match 24.2%; Score 24; DB 1; Length 20;  
 Best Local Similarity 35.7%; Pred. No. 9.3e+03;  
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 SSDGWNNTQQLF 14  
 Db 2 ASISLYNSNTISYF 15

RESULT 36  
**OMP\_HAEGA**  
 ID OMP\_HAEGA STANDARD; PRT; 20 AA.  
 AC P80451;  
 DT 10-OCT-2003 (Rel. 42, last sequence update)  
 DT 05-OCT-2003 (Rel. 42, last annotation update)  
 DE Major outer membrane protein (MOMP) (Outer membrane protein H)  
 (Fragment).  
 DB Name=ompH;  
 GN Haemophilus gallinarum.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 NCBI\_TAXID=728;  
 [1] SEQUENCE, AND SUBCELLULAR LOCATION.  
 RC STRAIN=IDPH 1645 / Serovar A1;  
 RX MEDLINE=96434400; PubMed=8837367;  
 RA Hartmann L., Schroeder W., Luebke-Becker A.;  
 RT "A comparative study of the major outer membrane proteins of the avian  
 Haemophilus and Pasteurella gallinarum.",  
 RL Zentralbl. Bakteriol. 284:47-51(1996).  
 CC -!- FUNCTION: Structural rigidity of the outer membrane of elementary  
 bodies and porin forming, permitting diffusion of solutes through  
 the intracellular reticulate body membrane.  
 CC -!- SUBUNIT: Disulfide bond interactions within and between MOMP  
 molecules and other components form high molecular-weight  
 oligomers.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
 CC -!- SIMILARITY: Belongs to the Gram-negative porin family.  
 KW Direct protein sequencing; Outer membrane; Porin; Transmembrane.  
 FT NON\_TER 20  
 SEQUENCE 20 AA; 2142 MW; 2B0C2CED4FEB635CB CRC64;

Query Match 24.2%; Score 24; DB 1; Length 20;  
 Best Local Similarity 44.4%; Pred. No. 9.3e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 37  
**QY 5 LWANNQTL 13**  
 Db 3 VYNNEGTQV 11

RESULT 37  
**QY 51950**  
 PRELIMINARY; PRT; 20 AA.  
 AC 051950;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DB Major outer membrane protein (Fragment).  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 NCBI\_TAXID=813;  
 RX SEQUENCE FROM N.A.  
 MEDLINE=98055742; PubMed=9395364;

Query Match 24.2%; Score 24; DB 1; Length 20;  
 Best Local Similarity 35.7%; Pred. No. 9.3e+03;  
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

RESULT 38  
**QY 601952**  
 PRELIMINARY; PRT; 20 AA.  
 AC 051952;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Outer membrane protein (Fragment).  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiaceae; Chlamydia.  
 NCBI\_TAXID=813;  
 RX SEQUENCE FROM N.A.  
 RA Bobo L., Novak N.G.;  
 RT "Severe disease in children with trachoma is associated with  
 persistent Chlamydia trachomatis infection.";  
 RL J. Infect. Dis. 00-0-0(1998);  
 DR EMBL; AF015550; AAB95378.1; -.  
 FT NON\_TER 1  
 SEQUENCE 20 AA; 2223 MW; D838044775219589 CRC64;  
 Query Match 24.2%; Score 24; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 9.3e+03;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 NNNTQQL 13  
 Db 2 NENQTKV 8

RESULT 39  
**QY 77044775219589**  
 PRELIMINARY; PRT; 20 AA.  
 ID Q77044775219589  
 AC 077044775219589;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 05-TUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE UORF3 (UORF1).  
 GN Name=Biffa;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TAXID=10090;  
 RN [1] SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 STRAIN=BALB/c;  
 RA Jenkins Z.A., Johansson R.E.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY129324; AACN17524.1; -.  
 DR EMBL; AY129326; AACN17529.1; -.

DR EMBL; AY129329; AAM17536.1; - .  
 DR GO; GO:0005377; Cytoplasm; IDA.  
 DR GO; GO:005634; C:nucleus; IDA.  
 DR GO; GO:0006915; P:apoprotein; IDA.  
 SQ SEQUENCE 20 AA; 2265 MW; E3C2BPF800E00F3F CRC64;  
 Query Match 24.2%; Score 24; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 9.3e+03; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 3; Mismatches 0;  
 QY 4 GLWANN 9 ||||:  
 Db 9 GLWSSS 14  
 RESULT 40  
 Q90X92 PRELIMINARY; PRT; 20 AA.  
 ID Q90X92;  
 AC 090X92;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Tyrosinase (Fragment).  
 Name=TYR.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Deng X., Yang Y., Liu W.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF416915; AAL14561.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2300 MW; AD237P25FA1BA696 CRC64;  
 Query Match 24.2%; Score 24; DB 2; Length 20;  
 Best Local Similarity 44.4%; Pred. No. 9.3e+03; 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 2; Mismatches 3;  
 QY 5 DANNNOTL 13 ||||:  
 Db 11 TWANIQSL 19  
 Search completed: December 30, 2004, 16:31:25  
 Job time : 192 secs